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OM nucleic - nucleic search, using SW model

Run on: June 26, 2002, 15:31:43 ; Search time 3987.01 Seconds
(without alignments)
11526.100 Million cell updates/sec

Title: SEQMOD
Perfect score: 2196
Sequence: I aatccgagcagcattgtgaa.....acccagtagctctctgctcta 2196

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1797656 seqs, 10463268293 residues
Total number of hits satisfying chosen parameters: 3595312

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: gb_ba:*
2: gb_hlg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sy:*
12: gb_un:*
13: gb_vl:*
14: gb_vl:*
15: em_ba:*
16: em_fun:*
17: em_hum:*
18: em_in:*
19: em_mu:*
20: em_om:*
21: em_or:*
22: em_ov:*
23: em_pat:*
24: em_ph:*
25: em_pl:*
26: em_ro:*
27: em_sts:*
28: em_un:*
29: em_vl:*
30: em_hlg_hum:*
31: em_hlg_inv:*
32: em_hlg_other:*
33: em_hlgo_inv:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query	Score	Match	Length	ID	Description
1	HSU09806	2196	6	6	6	2196 bp mRNA linear SYN 06-DEC-1999

1	2186.6	99.6	2196	12	HSU09806	U09806 Synthetic c
2	2186.6	99.6	2219	6	A47328	A47328 Sequence 3
3	2186.6	99.6	2219	6	AR097969	AR097969 Sequence
4	2186.6	99.6	2219	6	AR145811	AR145811 Sequence
5	2186.6	99.6	2219	6	AX356174	AX356174 Sequence
6	2186.6	99.6	2220	6	A47326	A47326 Sequence 1
7	2186.6	99.6	2220	6	AR097968	AR097968 Sequence
8	2186.6	99.6	2220	6	AR145810	AR145810 Sequence
9	2186.6	99.6	2220	6	AX356172	AX356172 Sequence
10	2177.6	99.2	2187	6	AR144956	AR144956 Sequence
11	2177.6	99.2	2187	6	AX050441	AX050441 Sequence
12	2177.6	99.1	2313	6	HS237672	HS237672 Homo sapi
13	1961.6	89.3	1250	10	AX069359	AX069359 Sequence
14	887.4	40.4	1250	10	RN057049	U57049 Rattus norv
15	447.6	20.4	551	4	AF239166	AF239166 Sus scrof
16	434.4	19.8	533	4	AF007464S11	AF105987 Homo sapi
17	434.4	19.8	159273	2	AC025001	AC025001 Homo sapi
18	275.6	12.6	2225	8	AF174486	AF174486 Zea mays
19	271	12.3	2034	8	AF370515	AF370515 Arabidops
20	269.4	12.3	1917	8	AF181967	AF181967 Arabidops
21	269.4	12.3	1917	8	AY050434	AY050434 Arabidops
22	267.8	12.2	2037	8	AFH245414	AJ245414 Arabidops
23	255.4	11.6	341	9	H007464S05	AF105981 Homo sapi
24	255.4	11.6	470	11	G67550	G67550 csnpmthfr-P
25	243.6	11.1	81624	3	AC099763	AC099763 Caenorhab
26	242	11.0	346	9	H007464S01	AF105977 Homo sapi
27	242	11.0	4221	9	HS249275	AJ249275 Homo sapi
28	240.4	10.9	471	11	G67546	G67546 csnpmthfr-P
29	240.4	10.9	159273	2	AC025001	AC025001 Homo sapi
30	240.2	10.9	339	9	H007464S02	AF105978 Homo sapi
31	240.2	10.9	465	11	G67547	G67547 csnpmthfr-P
32	237.8	10.8	1994	8	AF181966	AF181966 Arabidops
33	237.8	10.8	2002	8	AY070034	AY070034 Arabidops
34	216	9.8	5069	2	AF260233	AF260233 Homo sapi
35	215.2	9.8	198544	2	AL606929	AL606929 Mus muscu
36	213.6	9.7	351	10	MMTHFR05	AF105992 Mus muscu
37	205.8	9.4	339	10	MMTHFR02	AF105989 Mus muscu
38	200	9.1	294	9	H007464S04	AF105980 Homo sapi
39	200	9.1	427	11	G67549	G67549 csnpmthfr-P
40	198.6	9.0	38570	3	U39849	U39849 Caenorhabdl
41	194	8.8	3082	8	SCYGL125W	722647 S.cerevisia
42	193.2	8.8	6812	8	SCSDP44GM	X44106 S.cerevisia
43	184.8	8.4	281	9	H007464S07	AF105983 Homo sapi
44	184.8	8.4	283	9	H007464S08	AF105984 Homo sapi
45	184.6	8.4	37093	8	SPAC56F8	269728 S.pombe chr

ALIGNMENTS

RESULT 1	HSU09806	2196 bp mRNA linear SYN 06-DEC-1999
LOCUS	Synthetic construct methylentetrahydrofolate reductase (MTHFR)	
DEFINITION	mRNA, complete cds.	
ACCESSION	U09806	
VERSION	U09806.2	GI:6174884
KEYWORDS		
SOURCE		
ORGANISM		
REFERENCE		
AUTHORS		
TITLE		
JOURNAL		
MEDLINE		
PUBMED		
REMARK		
REFERENCE		
AUTHORS		

Erratum: [[published erratum appears in Nat Genet 1994 Aug;7(4):551]]
2 (bases 1 to 2196)
Frost, P., Blom, H.J., Milos, R., Goyette, P., Sheppard, C.,

Db	1141	CGAACCCAGAGAGTGGAGCGAGATTCCCTAACGGCCCGCTGGGGCAATTCTCTTCCCTGCC	1200
QY	1201	tttgggagactctgaagactactactctcttaccitgaagacaagtcctcccaagagagag	1260
Db	1201	ttttggggagactggaagagactctactcttcttactctgaagagcaagtcctcccaagagagag	1260
QY	1261	ctctctgaagatctgtgggggagagagagctgancagtgatgaacaagtcctnagaagtccttggt	1320
Db	1261	ctctctgaagatctgtgggggagagagagctgancagtgatgaacaagtcctnagaagtccttggt	1320
QY	1321	ctttaccctctcgggagaagcaaacaccggaatggtacaaagtactgtgcctccttggagac	1380
Db	1321	ctttaccctctcgggagaagcaaacaccggaatggtacaaagtactgtgcctccttggagac	1380
QY	1381	gatagagcccccttgcgcgttgagacaagctctctgaagagagagctgcgtgcyggytgaaccgc	1440
Db	1381	gatagagcccccttgcgcgttgagacaagctctctgaagagagagctgcgtgcyggytgaaccgc	1440
QY	1441	caagygatcctcaccatcaactacacgcccacaatacaacgaggaagccgctctccgacccc	1500
Db	1441	caagygatcctcaccatcaactacacgcccacaatacaacgaggaagccgctctccgacccc	1500
QY	1501	atctgtaggctgggggccccagcgggggtatgcttcttcagaagagctacttaagatttctc	1560
Db	1501	atctgtaggctgggggccccagcgggggtatgcttcttcagaagagctacttaagatttctc	1560
QY	1561	acttcccgcgagacgaagcgaagacactctctcaagtgcctgaagagatcagagctccggtt	1620
Db	1561	acttcccgcgagacgaagcgaagacactctctcaagtgcctgaagagatcagagctccggtt	1620
QY	1621	aattaccacactgttcaatgttgaaggttgaacaatacaacaatgcctcctgaactgacgcg	1680
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QY	1681	aatgcctcacttgggggcaatcttccctgggcgagagatactccagcccacagctagtgat	1740
Db	1681	aatgcctcacttgggggcaatcttccctgggcgagagatctccagcccacagctagtgat	1740
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Db	1741	cccgtaagctcaatgltcttggaaagagagagcctttgccttgaattgaatgaatggagga	1800
QY	1801	aagctgatagaagagagatcccgctccgcagacatatccagatataccagacaactac	1860
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Db	1921	gaagacacacttgaagcttcttcaacaagagcccaaccbaaatgcygagaaagagagctcca	1980
QY	1981	tgagacctgcctctgaagcccttgcgttggagccaactcctgtccagccttccctccaca	2040
Db	1981	tgagacctgcctctgaagcccttgcgttggagccaactcctgtccagccttccctccaca	2040
QY	2041	gttgctgcttctcttgggaactcacaactcctctgtgtctctccaccccgagctccaactc	2100
Db	2041	gttgctgcttctcttgggaactcacaactcctctgtgtctctccaccccgagctccaactc	2100
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AA7328			

[illegible]

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Qy 541 gactgtgtgaagcaacacccgaagtgagtttggtgactaacttgacatctgtgtgagagtg 600
Db 541 GACCTGGTGAAGCACATCCGAAAGTGAGTTTGCTGACTTGTGACATCTGTGTGGCAGCT 600
Qy 601 taccocaaagccaccccgaaagcagggagccttgagagcttgagccttgaaacacttgagag 660
Db 601 TACCCCAAGGCGCACCCGGAAGCAGGAGCTTTGAGGCTGACCTGAACACTTGAAGAG 660
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Db 661 AAGGTGTGCGGGAGCGCGATTTTCATCATCAGCAGCTTTTCTTTGAGGCTGACACATTC 720
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Qy 781 ttccacacagggctacacactcccttcgagcagctgtgaaagctgtccaaagctgagagtg 840
Db 781 TTTCCCATCCAGGGCTACCACTCCCTTGCGCAGCTTGTGAAGCTTCCAAAGCTGAGGTG 840
Qy 841 ccacagagatcaagagcagtgatltgagccaatcaaagaacaaagatgctgcaatccgcaac 900
Db 841 CCACAGAGATCAAGAGAGATGATTGAGCCAAATCAAAAGAACAGATGTCATCCGCAAC 900
Qy 901 tatggcactgagcgtgagcgtgtgagcgtgtgagagagccttgcgcaagagtgctgtgtgca 960
Db 901 TATGGCATGAGCTGGCGGTGAGCCTGTGCCAGAGCTTGTGGCCATGAGCTGTGGTGCA 960
Qy 961 ggcctcaactcacaacctaaaccgagagatggtctacacagagtgctgaagcgctg 1020
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Db 1681 AATGCTGACTTGGGGATCTTCCCTGGGAGAGATCATCCAGCCACCGTAGTGAT 1740
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Db 1741 CCCGTCACTTCATGTTGTGAAGAGCAGAGCGCTTGGCCCTGTGATGACCGGTGGGGA 1800
Qy 1801 aagctgtatgagagagatcccgctcccgacacacacacacacacacacacacacacac 1860
Db 1801 AAGCTATGAGAGAGAGATCCCGTCCGACACATCATCATCATCATCATCATCATCATCAT 1860
Qy 1861 ttccgtgcaacacttgtagacaatgacttccacatgacacacacacacacacacacacac 1920
Db 1861 TTCCGTGCAACCTGTGTGAGACATGACTTCCCATGAGCAACTGCTCTGGCAGGTG 1920
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Db 2101 CCCAC 2160
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RESULT 3
AR097969
LOCUS AR097969 2219 bp DNA Linear PAT 14-FEB-2001
DEFINITION Sequence 3 from patent US 6074821.
ACCESSION AR097969
VERSION AR097969.1 GI:12807226
KEYWORDS
SOURCE
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 2219)
AUTHORS Rozen, R. and Goyette, P.
TITLE CDNA for human methylenetetrahydrofolate reductase
JOURNAL Patent: US 6074821-A 3 13-JUN-2000;
FEATURES
source 1..2219
BASE COUNT 501 a 657 c 620 g 441 t
ORIGIN

Query Match 99.6%; Score 2186.6; DB 6; Length 2219;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 2189; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
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Qy 361 gtgagctactgtgctcggagagacatctcgtgacatgacctgtgcgtcagcgctggag 420
Db 361 GTGACTACTGTGCTGCTGAGACCATCTGTCACATGACCTGCTGCCGTGACGCTGGAG 420
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Db 421 GAGATTCACGGGCCATCTGACAAAGCTAAGCAGCTGGCCCTGAAGAACATATGCGCGTG 480
Qy 481 cggagagaccccaatagatgagcagtgaggaagagagagagagcttcaactagcagtg 540
Db 481 CGGGAGAACCCAAATAGGTGACCACTGGGAAGAGAGAGGAGGCTTAACTAGCGAGTG 540
Qy 541 gacctgtgaaagcacaatccgaaagtgtgtgtgactacttggacatctgtgtggcagtg 600
Db 541 GACCTGTGGAAGCACAATCCGAAGTAGTGTGTGTGACTTGTGACATCTGTGTGGCAGGT 600
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Db 601 TACCCCAAGGCCACCCCGAAGCAAGAGCTTTGAGGCTGACCTGAACACTTGAAGAG 660
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Qy 841 ccaacagagatcaagagagctgtatgagccaatcaaaagcaagatgctgcacatccgacac 900
Db 841 CCACAGGAGATCAAGGAGGTATGAGCCAAATCAAAAGCAACGATGCTGCATCCGCAAC 900
Qy 901 taatgacatcagagctgagcgctgagacctgtgccaagagcttctgagcagtgagcttgtgca 960
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Db 1081 |||||

Db 1081 CGCCGAGAGGAAGATGATAGCTCCCATCTTCTGGGCTCCAGACCAAAAGATTACATCTAC 1140
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Db 1741 CCGGTCAAGCTCATGTCTCTGAAAGAGAGAGGCTTTTGCCCTGTGATTTGAAGCGGTGGGA 1800
Qy 1801 aagctgtatgagagagagctcccgctccgcaacatcaatccagtaacatccagcaactac 1860
Db 1801 AAGCTGTATGAGAGAGAGTCCCGTCCCGGACATCATTCAGTACATTCAGACAACTAC 1860
Qy 1861 ttctcgttcaacactgtgtgagacatgacttcccaatgaaacactgtccttgcagtggtg 1920
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RESULT 4
ARI45811 ARI45811 2219 bp DNA linear PAT 08-AUG-2001
LOCUS Sequence 3 from patent US 6218120.
DEFINITION ARI45811
ACCESSION ARI45811
VERSION ARI45811.1 GI:15109000
KEYWORDS
SOURCE
ORGANISM Unknown.
REFERENCE Unclassified.
1 (bases 1 to 2219)
AUTHORS Rozen, R. and Goyette, P.
TITLE Methods for detecting human methylene tetrahydrofolate reductase
JOURNAL Patent: US 6218120-A 3 17-APR-2001;
FEATURES
source 1..2219
location/Qualifiers
BASE COUNT 501 a 657 c 620 g 441 t
ORIGIN

Query Match 99.6%; Score 2186.6; DB 6; Length 2219;
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RESULT 5
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LOCUS AX356174
DEFINITION Sequence 3 from Patent WO0196598.
ACCESSION AX356174
VERSION AX356174.1 GI:18620687
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases)
AUTHORS Rozen, R.
TITLE Cdna for human methylenetetrahydrofolate reductase and uses thereof.
JOURNAL Patent: WO 0196598-A 3 20-DEC-2001;
MCGill University (CA)

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Source location/Qualifiers
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BASE COUNT 501 a 657 c 620 g 441 t
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Query Match 99.6%; Score 2186.6; DB 6; Length 2219;
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Best Local Similarity 99.7%; Pred. No. 0;
Matches 2189; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

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RESULT 6
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DEFINITION Sequence 1 from Patent WO9533054.
ACCESSION A47326
VERSION A47326.1 GI:2301334
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 2220)
AUTHORS Rozen, R. and Goyette, P.
TITLE cDNA FOR HUMAN METHYLENETHETRAHYDROFOLATE REDUCTASE
JOURNAL Patent: WO 9533054-A 1 07-DEC-1995;
UNIV MCGILL (CA)
COMMENT Other publication AU 2519895 951221.
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LOCUS AR097968 2220 bp DNA linear PAT 14-FEB-2001
DEFINITION Sequence 1 from patent US 6074821.
ACCESSION AR097968
VERSION AR097968.1 GI:12807225
KEYWORDS
SOURCE
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 2220)
AUTHORS Rozen,R. and Goyette,P.
TITLE CDNA for human methyltetrahydrofolate reductase
JOURNAL Patent: US 6074821-A 1 13-JUN-2000;
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LOCUS Sequence 1 from patent US 6218120.
ACCESSION ARI45810
VERSION ARI45810.1 GI:15108999
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 2220)
AUTHORS Rozen, R. and Goyette, P.
TITLE Methods for detecting human methylene tetrahydrofolate reductase
JOURNAL Patent: US 6218120-A 1 17-Apr-2001;
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location/Qualifiers
BASE COUNT 501 a 658 c 620 g 441 t
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Best Local Similarity 99.7%; Pred. No. 0;
Matches 2189; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

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LOCUS AX356172
DEFINITION Sequence 1 from Patent WO0196598.
ACCESSION AX356172
VERSION AX356172.1 GI:18620685
KEYWORDS
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ORGANISM human.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
1 (sites)
REFERENCE
AUTHORS Rozen, R.
TITLE Cdna for human methylenetetrahydrofolate reductase and uses thereof
JOURNAL Patent: WO 0196598-A 1 20-DEC-2001;
MCGill University (CA)
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Query Match 99.6%; Score 2186.6; DB 6; Length 2220;
Best Local Similarity 99.7%; Pred. No. 0;
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ACCESSION ARI44956
VERSION ARI44956.1 GI:15106823
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 2187)
AUTHORS Johnson, W.G. and Stenroos, E.Scott.
TITLE Methods for diagnosing, preventing, and treating developmental disorders due to a combination of genetic and environmental factors
JOURNAL Patent: US 6210950-A 1 03-APR-2001;
FEATURES
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	VERSION	AJ237672.1	GI:4753777			
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	AUTHORS	Homberger A., Linnebank M., Winter C., Rapp B. and Koch H.G.				
	TITLE	Revised transcription initiation site of the human methylenetetrahydrofolate reductase (MTHFR)				
	JOURNAL	Unpublished				
	REFERENCE	2 (bases 1 to 2313)				
	AUTHORS	Koch,H.G.				
	TITLE	Direct Submission				
	JOURNAL	Submitted (28-Mar-1999) Koch H.G., Stoffwechselabor, Univ. Kinderklinik, Albert-Schweitzer-Str. 33, Muenster 48149, GERMANY				
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Qy	1569	cgagacagcggaagacactctcgaagtctgtaagaagtaagacgcgcggttaattacca	1628
Db	1686	CGAGACAGCGGAGAGCACTTCTCAGGTGCTGAAGAAGTACAGAGCTCCGGTTAATTACCA	1745
Qy	1629	cctgtlcaatgtgaaggttgaagaacatcaacaatgccccctgaactcgosgcgaaatgtgt	1688
Db	1746	CTTTCTCAATGTGAAGGGGTGAAGAAATCAACCAATCCCCCTGAAACGCAAGCGAAATGCTGT	1805
Qy	1689	gaatttggggacatcttcctccgtggcgagaagatcatccgaagcccaagtaagtatcccgtaag	1748
Db	1806	CACTTGGGGCACTTCTTCCCTGGGCGAGAGATCTTCAGAGCCCACTGATGTGATCCGCTGAG	1865
Qy	1749	cttcatlgtlcttggaaagaaaggacgttcttgcccctgtagatagaacgttgggaaagctgta	1808
Db	1866	CTTCAATGTCTGTGAAGAGAGAGCCCTTTGGCCCTGTGAGTATGAGCGGTGGGAAACCTGTA	1925
Qy	1809	tgaagaaagatccccggtcccgaccatataccagtaacatccagcaactacttcttgt	1868
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Qy	1869	caacctgtgtgaaacatgaacttcccaactggacaacatctgaccttgcagagtgtgtgaagaac	1928
Db	1986	CAACCTGTGTGACAAATGACTTCCCACTGGACAACTGCTCTGGCAGGTGTGAAGACAC	2045
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Qy	1989	cgctccgaagccctgctgttggagccaactcgttccgcgacctctcctccacagtgctgt	2048
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Qy	2049	tctcttgggaactccaacttctcttgcgtgtcttcccaaccgggacctccaactccccacct	2108
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Qy	2109	gacaaatggagacttagactctgtagttagaggtcttccagctcttcttgaacctgtagtggcccc	2168
Db	2226	GACAAATGGAGCTAGACTGAGTGAAGGCTTCCAGGCTTCTTGAGACCTGAATCGGCCCC	2285
Qy	2169	acatgggaacctagtaactctctgtcctta	2196
Db	2286	ACATGGGAACCTAGTACTCTGTGCTCTA	2313
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LOCUS	AX069359	1971 bp	DNA linear PAT 25-JAN-2001
DEFINITION	Sequence 23 from Patent WO0102600.		
ACCESSION	AX069359		
VERSION	AX069359.1	GI:12579222	
KEYWORDS	human.		
SOURCE	human.		
ORGANISM	Homo sapiens		
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		

REFERENCE	1 (bases 1 to 1971)	Mammalia: Eutheria; Primates; Catarrhini; Hominiidae; Homo.
AUTHORS	Yuan,C.S.	
TITLE	Detection of analytes using attenuated enzymes	
JOURNAL	Patent: WO 0102600-A 23 11-JAN-2001;	
FEATURES	GENERAL ATOMICS (US)	
SOURCE	Location/Qualifiers 1..1971 /organism="Homo sapiens" /db_xref="taxon:9606" /note="Human methyltetrahydrofolate reductase (MTHFR) gene: exons 1-8"	
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QY	73 agtgcagtgagagcttcccaagaatagttcgaatgtttccaccgcggccttgaccctgag	132
DB	61 ACTGCAGTGAAGAGCTCCAAAGATAGTTGCAATGTTCACACCCCGGCGCTGAGACCTTAG	120
QY	133 cggcatgagaagctccggagagaagatgagcggcgatgtgaatctgtggaagaagtggttc	192
DB	121 CGGCATGAAGAGACTCCGGAGAGATGAGGCGCGCATTTGGAACTGTGTACAAAGTGGTTC	180
QY	193 tccctggaattcttcctctcgaactgtctgagggagagctgtcaatcattcaatgagttt	252
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QY	313 cctgtgcacagaagaagagccctctctcatgatgatcgcagacagacgcgctgaactactgt	372
DB	301 CCTGCTCAGACAGAGAGACGCTCTCTCATATGATGATGCCAGCAGCGCGTGAACTACTGT	360
QY	373 ggccttgagaaacatcctgtcacatgacatgcgtgcgcgcagcgttgagaagatacagggc	432
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QY	433 catctgcacaaagctcraagcagctgggcctcgaagaacatcatgtgcgttgaggagaacca	492
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D	b	9	61	TACACCTCAACCCCGAGATGGCTACACAGAGGTGCTGAAGGCGCTGGGGATGTGGACT	1020
O	y	1	03	gagagccccaaaggtgtcccttaacctgtgcctctaagtgcacacccccaaagcgccgaagaa	1092
D	b	1	21	GAGGACCCCAAGGCGCTCCCTTAACCTGGGGCTCTGAGTGCACCCCAAGCGCCGAGAAGAA	1080
O	y	1	93	gattgaagctcccaactctctctgagcctccagaaccaaaagattacatactaccgtaccagaag	1152
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D	b	1	261	TGGGGGGGAGGAGCTGAGACAGTGAAGCAAGTGTCTTGAAGTCTTGTCTTACCTCTCG	1320
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D	b	1	321	GGAGAACCAAAACCGGAATGCTCAACAAAGTACTGTGCTGTGCTCGAGACGATAGCCCTCG	1380
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D	b	1	381	GCGGCTGAGACCAACCTGCTGAAGAGAGAGCTCTCGGGGTGAACCGCAGGGCATTCCTC	1440
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D	b	1	741	ATGTCTCTGGAAGAGCGAGGCTTGTGCTCTGTGATTGAACGGGTGGGAAAGCTGTATAG	1800
O	y	1	813	gaggagctcccgcttccgcacacatcacatccagtgatcatcacagaacaactcttctgtctaac	1872
D	b	1	801	GAGGAGTCCCGCTCCGACCATCATCTCAGTACATCAAGACATCACTTCTGTGTTAAC	1860
O	y	1	873	ctggttgaacaatgacttcccaactggaacaactgctcttgcaggtgtgtgaagaacatctg	1932

Db 1861 CTGTGGCAATGACTTTCCCACTGGACACATGCTCTTGGCGAGTGTGTGGAGACACATTG 1920

Qy 1933 gagcttctcaacagggccccaccagaaatcgagagaaacggagagcttcacatga 1983

Db 1921 GAGCTTCTCAACAGGCCCCACCGAATGCGAGAGAAACGGAGCTTCATTGA 1971

RESULT	14
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LOCUS	RNU57049
DEFINITION	1250 bp mRNA linear ROD 05-JUN-1996 Rattus norvegicus methyltetrahydrofolate reductase mRNA, partial

VERSION	U57049.1	GI:1354771
KEYWORDS		
SOURCE	Rattus norvegicus strain-Wistar.	
ORGANISM	Rattus norvegicus	

REFERENCE 1 (pages 1 to 1250)
AUTHORS Li, Z., Chen, K. H., Zhang, C. H., Zhu, H. P., Meng, Z. H. and Tang, J
TITLE Direct Submission
JOURNAL
Submitted (29-MR-1996) J. Tang, The Institute of Cardiovascular

Research, Beijing Medical University, Xue-Yuan Lu, Beijing, Beijing
100083, P. R. China

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FEATURES      Location/Qualifiers
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two primers used in RT-PCR was designed based on the sequence of human methylenetetrahydrofolate reductase"

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BASE COUNT	300	350	360	240
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Db 237 TTTGACCGGTTGGGGGGAGGGGGCCCTTCCTTGTGATGTTACCTGGTTACCCAGGTGGC 296

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OY		370	tatggccttgagacacattccctgcacatatccctgtcgcctgaacgcccttggaaagtacag	429
Db		356	TGTTGCTTGGAAACATCTCGACATGACCTGGCTGCCAGCAGCCGCAGAGAGATCTCA	415
OY		430	ggccatctgcacaagaattaagcagctgtggccttgaagaaacatalqgcgttgcgggsaac	489
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OY		610	ggcaccaccccgaacaggaagccttggagcgtgcacttgaagaagcattgaagagaaggttnt	669
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Db		656	GCAGGGCCGCACTTATCATCACTCAGCTCTCTTTGAGGGAGAGCGCTCTTCCAGCTTC	715
OY		730	gtlaaaggcatgcacagcaattgggcatcaacttggccccatgtcccggaacttcctccatc	789
Db		716	GTGAAGGCGTGGCAACATAGGCATCTCCTGCCCTATCTCGCTGGGATCTTCCCTATC	775
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Db		896	GAGCTGTGCTGAMACTTGTGCCGGGAACGTGGACAGTGGCTGTGGTGC GGCGCTCCAC	955
OY		970	ttctacacctcaacggcgagatgtgtactacaagaag- gftgcgtgaacgctgtggatgtg	1028
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OY		1029	gactaagaagcccaaggcgtccctcaactcgtgcctcaatgtgcacacccaagagcgccgaga	1088
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OY		1209	gctgaagactactaccccttctactctgaagagcaagtcccccagaaggagct	1262
Db		1196	GCTGAAGACTACTACCTCTTCTACTGTAAAAAGCAAGTCCCACAGAGAGAACT	1249

RESULT	15
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DEFINITION	Sus scrofa methyltetrahydrofolate reductase (MTHFR) mRNA,
ACCESSION	partial cds.
VERSION	AF239166
KEYWORDS	AF239166.1 GI:7716550
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SOURCE	Pig.
ORGANISM	Sus scrofa
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS	Mammalia; Eutheria; Cetartiodactyla; Suidae; Sus.
TITLE	1 (bases 1 to 551)
JOURNAL	Vallée,M., Palin,M.-F.F., Guay,F., Beaudry,D., Blouin,R.,
REFERENCE	Laforest,J.-P.P., Lessard,M. and Matte,J.
TITLE	Effect of folic acid supplement, breed and parity of sows on folate
JOURNAL	metabolism gene expression in early pregnancy
REFERENCE	Unpublished
TITLE	2 (bases 1 to 551)
JOURNAL	Vallée,M., Palin,M.-F.F., Guay,F., Beaudry,D., Blouin,R.,
REFERENCE	Laforest,J.-P.P., Lessard,M. and Matte,J.
TITLE	Direct Submission
JOURNAL	Submitted (25-FEB-2000) Agriculture and Agri-Food Canada Dairy and
REFERENCE	Swine Research and Development Centre, P.O. Box 90, 2000 Route 108
TITLE	East, Lennoxville, Quebec J1M 1Z3, Canada
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 Db 541 ATGAGGCCGCC 551

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18: /SIDSI/gcgdata/geneseq/geneseq-emb1/NA1998.DAT:*
19: /SIDSI/gcgdata/geneseq/geneseq-emb1/NA1999.DAT:*
20: /SIDSI/gcgdata/geneseq/geneseq-emb1/NA2000.DAT:*
21: /SIDSI/gcgdata/geneseq/geneseq-emb1/NA2001A.DAT:*
22: /SIDSI/gcgdata/geneseq/geneseq-emb1/NA2001B.DAT:*
23: /SIDSI/gcgdata/geneseq/geneseq-emb1/NA2002.DAT:*
24: /SIDSI/gcgdata/geneseq/geneseq-emb1/NA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2186.6	99.6	2219	22	AAD20463 Human methylenetet
2	2186.6	99.6	2220	21	AAA50633 Human methylenetet
3	2186.6	99.6	2220	22	AAD20462 Human methylenetet
4	2185	99.5	2219	17	AAT09689 Human methylene-te
5	2185	99.5	2220	17	AAT09694 Human methylene-te
6	2177.6	99.2	2187	22	AAC91206 Human methylenetet
7	1089.6	49.6	3283	21	AAA50634 Mouse methylenetet
8	452.2	20.6	3181	21	AAA50635 Mouse methylenetet
9	434.4	19.8	532	22	AAD20485 Human MTHFR gene e

C	10	434.4	19.8	23748	22	AA105229 Human reproductiv
	11	269.4	12.3	1942	21	AAC49168 Arabidopsis thalia
	12	255.4	11.6	341	22	AAD20479 Human MTHFR gene e
	13	250.8	11.4	1821	21	AAC43311 Arabidopsis thalia
	14	242	11.0	346	22	AAD20475 Human MTHFR gene e
	15	240.2	10.9	339	22	AAD20476 Human MTHFR gene e
	16	213.6	9.7	351	22	AAD20480 Mouse MTHFR gene e
	17	205.8	9.4	339	22	AAD20487 Arabidopsis thalia
	18	200.6	9.1	1335	21	AAC36967 Arabidopsis thalia
	19	200	9.1	294	22	AAD20478 Human MTHFR gene e
	20	184.8	8.4	281	22	AAD20481 Human MTHFR gene e
	21	184.8	8.4	283	22	AAD20482 Human MTHFR gene e
	22	181	8.2	343	22	AAD20486 Mouse MTHFR gene e
	23	172.8	7.9	1493	21	AAC44829 Arabidopsis thalia
	24	160	7.3	427	22	AAD20496 Mouse MTHFR gene e
	25	152.4	6.9	6727	24	AB133296 Human immune syste
	26	150.8	6.9	294	22	AAD20489 Mouse MTHFR gene e
	27	148	6.7	276	22	AAD20492 Mouse MTHFR gene e
	28	148	6.7	283	22	AAD20493 Mouse MTHFR gene e
	29	146	6.6	147	21	AA440624 Human MTHFR normal
	30	139.8	6.4	235	22	AAD20480 Human MTHFR gene e
	31	135	6.1	6727	24	AB133297 Human immune syste
	32	130	5.9	144	21	AA440625 Human MTHFR HC fra
	33	124.2	5.7	220	22	AAD20484 Human MTHFR gene e
	34	120	5.5	235	22	AAD20491 Mouse MTHFR gene e
	35	119	5.4	120	22	AAD11821 Methylenetetrahydr
	36	115.2	5.2	210	22	AAD20477 Human MTHFR gene e
	37	114.8	5.2	558	21	AA250061 Soybean 5,10-methy
	38	106.2	4.8	202	22	AAD20483 Human MTHFR gene e
	39	99.6	4.5	219	22	AAD20495 Mouse MTHFR gene e
	40	91.4	4.2	876	24	AA597261 Neisseria meningit
	41	88.6	4.0	211	22	AAD20488 Mouse MTHFR gene e
	42	81.8	3.7	349980	21	AAF21609 Neisseria meningit
	43	79	3.6	80	22	AAH02417 Human MTHFR coding
	44	77.4	3.5	80	22	AAH02418 Human MTHFR coding
	45	74.6	3.4	759	21	AA481845 N. meningitidis pa

ALIGNMENTS

RESULT	1
ID	AAD20463 standard; cDNA; 2219 BP.
XX	XX
AC	AAD20463:
XX	XX
DT	03-JAN-2002 (first entry)
XX	XX
DE	Human methylenetetrahydrofolate reductase (MTHFR) protein cDNA #2.
XX	XX
KW	Human; methylenetetrahydrofolate reductase; MTHFR; gene therapy; glioma; antilease therapy; EC 1.5.1.20; chromosome 1p36.3; cancer; kidney cell;
KW	pancreas; lung; brain; cytosolic; colon carcinoma; breast; colorectal;
KW	neuroblastoma; leukaemia; ss.
XX	XX
OS	Homo sapiens.
XX	XX
FH	Key
FT	CDS
FT	13..1983
FT	/*tag- a
FT	/product- "Human methylenetetrahydrofolate reductase
FT	(MTHFR) protein"
FT	/EC_number- "1.5.1.20"
XX	XX
PN	US2001025030-A1.
XX	XX
PD	27-SEP-2001.
XX	XX
PF	01-DEC-2000; 2000US-0728910.
XX	XX
PR	01-MAR-1999; 99US-0258928.
XX	XX

(ROZE/) ROZEN R.
 (SEKH/) SEKHON J.
 Rozen R, sekhn J;
 WPI: 2001-638509/73.
 P-PSDB: AAL12607.
 New antisense nucleic acids, which are methyltetrahydrofolate
 reductase inhibitors, useful for treating, stabilizing or preventing
 cancer, e.g. breast carcinoma, colon carcinoma, colorectal carcinoma or
 neuroblastoma
 Disclosure: Fig 6; 68pp; English.
 The invention relates to a non allele-specific antisense nucleic acids,
 which binds to methyltetrahydrofolate reductase (MTHFR; EC 1.5.1.20)
 nucleic acids and inhibits MTHFR protein expression in a mammal. MTHFR
 catalyses the NADPH-linked reduction of 5,10-methyltetrahydrofolate to
 5-methyltetrahydrofolate, a co-substrate for methylation of
 homocysteine to methionine. The invention provides potential therapy for
 individuals with MTHFR deficiency. The non allele-specific antisense
 nucleic acids are useful for treating, stabilizing or preventing cancer,
 particularly breast carcinoma, colon carcinoma, colorectal carcinoma,
 lung cancer, brain cancer, pancreatic cancer, kidney cell cancer,
 neuroblastoma, glioma and leukemia. MTHFR cDNA probe is used in gene
 therapy. The present sequence is human methyltetrahydrofolate
 reductase (MTHFR) protein cDNA #2. Human MTHFR gene is mapped to
 chromosome 1p36.3.
 Sequence 2219 BP; 501 A; 657 C; 620 G; 441 T; 0 other:

Query Match	99.6%	Score 2186.6	DB 22	Length 2219
Best Local Similarity	99.7%	Pred. No. 0		
Matches 2189, Conservative	0	Mismatches 7	Indels 0	Gaps 0
QY 1 aattccggaagcatgattgacgcaagccaaaggaagaacagacgtctaaacctgttgag 60				
Db 1 aattccggaagccattggttgacgaagccaaaggaagaacagacgtctaaacctgttgag 60				
QY 61 ggcagltgcagacagatgycagatgagagcttcacaaagatagtgtctgagatgtgtccaccccgagc 120				
Db 61 ggcagltgcagacagatgycagatgagagcttcacaaagatagtgtctgagatgtgtccaccccgagc 120				
QY 121 ctggagccctgagcggcattgagagagatctccgggagaagatgagcggcggatctggaatctggt 180				
Db 121 ctggagccctgagcggcattgagagagatctccgggagaagatgagcggcggatctggaatctggt 180				
QY 181 gacaaagtgtctccctgtgaattcttccctctgaacagctcgagggagacgttcaatctc 240				
Db 181 gacaaagtgtctccctgtgaattcttccctctgaacagctcgagggagacgttcaatctc 240				
QY 241 atctcaaggtttgacacggatgagcagcaggtgcccctctacatagacgtgacgtcgagac 300				
Db 241 atctcaaggtttgacacggatgagcagcaggtgcccctctacatagacgtgacgtcgagac 300				
QY 301 ccaggaagttgacccctggtgtccagacaaggaagacatctctccaagtatgcgacagccgc 360				
Db 301 ccaggaagttgacccctggtgtccagacaaggaagacatctctccaagtatgcgacagccgc 360				
QY 361 gtgaactactgtgacctgagagacacatctctgacacatgacactgtgcgcgccaagcgcttgag 420				
Db 361 gtgaactactgtgacctgagagacacatctctgacacatgacactgtgcgcgccaagcgcttgag 420				
QY 421 gagatcacgggccaatctgcacaaagctlaagcagcttgggcctgagaggaaatcatgctgctg 480				
Db 421 gagatcacgggccaatctgcacaaagctlaagcagcttgggcctgagaggaaatcatgctgctg 480				
QY 481 cggggagagcccaataatggtgacacagatggggaagaagagaugagaagcttcaactacgcaatg 540				
Db 481 cggggagagcccaataatggtgacacagatggggaagaagagaugagaagcttcaactacgcaatg 540				

QY	541	gaacctgctgaaagacaatccgaagctgagttctgtgactactcttgacatctgtgtgcagct	600
Db	541	gaaactctgtgaagacaatccgaagctgagttctgtgactactcttgacatctgtgtgcagct	600
QY	601	taccccaaaagcgacaccccgaaagcaggtgctcttgagctgtgacccctgaaagcacttgaaagag	660
Db	601	taccccaaaagcgacaccccgaaagcaggtgctcttgagctgtgacccctgaaagcacttgaaagag	660
QY	661	aaggtgtntgtgcggagccgaattcaatcatcagcagctcttctcttgagctgacacatc	720
Db	661	aaggtgtctcgcggagcgagattcaatcatcagcagctcttctcttgagctgacacatc	720
QY	721	tccgcgttctgtaaaagcatctgcacgaacatctggcatcaattggcccccatcgcgcgcgggac	780
Db	721	tccgcgttctgtaaaagcatctgcacgaacatctggcatcaattggcccccatcgcgcgcgggac	780
QY	781	ttcccatccagggctacacacacccctctcgcgagagctgtgtaaagctgttccaaagctgtgaag	840
Db	781	ttcccatccagggctacacacacccctctcgcgagagctgtgtaaagctgttccaaagctgtgaag	840
QY	841	ccaacagggatataaagacgtgattgagccaatacaagaacagatgtctgcacccgaaac	900
Db	841	ccaacagggatataaagacgtgattgagccaatacaagaacagatgtctgcacccgaaac	900
QY	901	tatgtgcatccagctctgcgcgtgagccgtctgcgcgaaggaagctctctgcgaatctgtgtgca	960
Db	901	tatgtgcatccagctctgcgcgtgagccgtctgcgcgaaggaagctctctgcgaatctgtgtgca	960
QY	961	ggctcccaactcttacaacccctcaacccgcgagatgtgtctacacagagatgtctgaagccgtg	1021
Db	961	ggctcccaactcttacaacccctcaacccgcgagatgtgtctacacagagatgtctgaagccgtg	1021
QY	1021	ggagatctggaactgaaagaccccgagcgctcccccataccctgcgcgtccagctgtgcaccccaag	1081
Db	1021	ggagatctggaactgaaagaccccgagcgctcccccataccctgcgcgtccagctgtgcaccccaag	1081
QY	1081	cgcgcgaagaaagatgtacgtccacactctctggcctccagacccaagaaagtatacatctac	1141
Db	1081	cgcgcgaagaaagatgtacgtccacactctctggcctccagacccaagaaagtatacatctac	1141
QY	1141	cgtaccccaagggctgtagaagaaattccccataacgcgcgcgtggggagaaattcccttcacccctg	1201
Db	1141	cgtaccccaagggctgtagaagaaattccccataacgcgcgcgtggggagaaattcccttcacccctg	1201
QY	1201	ttctgggagactgaaagacatacatcctctctacaccttgaaagacaagctcccccagaagagag	1261
Db	1201	ttctgggagactgaaagacatacatcctctctacaccttgaaagacaagctcccccagaagagag	1261
QY	1261	ctgctcgaagatgtgtagggagaaagctgaaacagctgaaagacaagtctcttmaagctttgtt	1321
Db	1261	ctgctcgaagatgtgtagggagaaagctgaaacagctgaaagacaagtctcttmaagctttgtt	1321
QY	1321	ctttaaactctctgggaaagaaacccaacccgaaatctgttcaacaagaatctgacctgcgcctggaac	1381
Db	1321	ctttaaactctctgggaaagaaacccaacccgaaatctgttcaacaagaatctgacctgcgcctggaac	1381
QY	1381	gataagacccctgcgcgtctgaaagacagccgtctgtgaagaaagatcgtctgcgcgggtgaaacgc	1441
Db	1381	gataagacccctgcgcgtctgaaagacagccgtctgtgaagaaagatcgtctgcgcgggtgaaacgc	1441
QY	1441	cagggaatccctcacacatacaatcaacgaaccccaaaatcaacgggaaagcgcgtccctccgaaccc	1501
Db	1441	cagggaatccctcacacatacaatcaacgaaccccaaaatcaacgggaaagcgcgtccctccgaaccc	1501
QY	1501	atcgtggtgctgtagcccccagccggtgtagtcttccagagaagcctactaagatgttttc	1561
Db	1501	atcgtggtgctgtagcccccagccggtgtagtcttccagagaagcctactaagatgttttc	1561
QY	1561	acttcccgcgagaaagacgggaagcaactctctgcaagctgtctgaagaagtacagatcccggtt	1621
Db	1561	acttcccgcgagaaagacgggaagcaactctctgcaagctgtctgaagaagtacagatcccggtt	1621
QY	1621	aattacaaccttgcaatgtgaaaggggtgaaaaacatcaacaaatgcacctgaaactgcgaaccc	1681


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Db      1621 aattaccacctgtcattgtgaagggtgaataacatccactgacctgaactgcagccg 1680
Oy      1681 aatgcgtacctggggacatctccctgggagagatcatccagcccgtaagtgat 1740
Db      1681 aatgcgtacctggggacatctccctgggagagatcatccagcccgtaagtgat 1740
Oy      1741 cccgctcaactcgtctcgtgaagagagagcccttgcccttgatagtcggtgggga 1800
Db      1741 cccgctcaactcgtctcgtgaagagagagcccttgcccttgatagtcggtgggga 1800
Oy      1801 aagcttataagagagagagcccgctccgaccatcatccatataccacgacaactac 1860
Db      1801 aagcttataagagagagagcccgctccgaccatcatccatataccacgacaactac 1860
Oy      1861 ttccctgtcaacctgtgtgaacatgacttccacttgacaactgacctgtgcagtggtg 1920
Db      1861 ttccctgtcaacctgtgtgaacatgacttccacttgacaactgacctgtgcagtggtg 1920
Oy      1921 gaagacacattgagacttctcaacagcccaaccagaatgcgagagaacgaggtctca 1980
Db      1921 gaagacacattgagacttctcaacagcccaaccagaatgcgagagaacgaggtctca 1980
Oy      1981 tgaccctgctccttgacgcccctgtgtgagaccactcgtccgctctcctctccaca 2040
Db      1981 tgaccctgctccttgacgcccctgtgtgagaccactcgtccgctctcctctccaca 2040
Oy      2041 gtcgtctctctcttggaactcactctcctctgtgtctctccacccggctccactc 2100
Db      2041 gtcgtctctctcttggaactcactctcctctgtgtctctccacccggctccactc 2100
Oy      2101 cccacactgacatgacgactagactgcgagtgaggtctccaggtctcctgacctgag 2160
Db      2101 cccacactgacatgacgactagactgcgagtgaggtctccaggtctcctgacctgag 2160
Oy      2161 tcggccccacatgggaacctagactctctgtctcta 2196
Db      2161 tcggccccacatgggaacctagactctctgtctcta 2196

RESULT 2
AAAS0633 ID AAAS0633 standard; cDNA: 2220 BP.
AAAS0633:
AC      19-DEC-2000 (first entry)
DX
XX
DE      Human methylenetetrahydrofolate reductase cDNA.
XX
KW      Methylenetetrahydrofolate reductase; MTHFR; human; folic acid;
KW      cardiovascular disorder; cancer; neuroblastoma;
KW      colorectal carcinoma; osteoporosis; neural tube
KW      neurological disorder; gene therapy; diagnosis; chromosome 1p36.3;
KW      ss.
XX
OS      Homo sapiens.
XX
FH      Key Location/Qualifiers
FT      CDS 13..1983
FT      /*tag- a
FT      /EC_number= "1.5.1.20"
FT      mutation replace(167,A)
FT      /*tag- b
FT      mutation replace(482,A)
FT      /*tag- c
FT      mutation replace(559,T)
FT      /*tag- d
FT      mutation replace(677,T)
FT      /*tag- e
FT      mutation replace(692,T)
FT      /*tag- f
FT      mutation replace(764,T)

```

```

FT      mutation /*tag- g
FT      replace(792+1,A)
FT      /*tag- h
FT      mutation replace(985,T)
FT      /*tag- i
FT      mutation replace(1015,T)
FT      /*tag- j
FT      mutation replace(1018,T)
FT      /*tag- k
FT      mutation replace(1298,C)
FT      /*tag- l
FT      mutation replace(1317,C)
FT      /*tag- m
PN      WO200052205-A2.
XX
XX      08-SEP-2000.
XX
XX      28-FEB-2000; 2000WO-IB00442.
XX
XX      01-MAR-1999; 99US-0258928.
XX
XX      (UWMC-) UNIV MCGILL.
XX
XX      Rozen R, Goyette P;
XX      WPI; 2000-572192/53.
XX
XX      P-PSDB; AAY96186.
XX
XX      cDNA probe for the human methylenetetrahydrofolate reductase (MTHFR),
XX      useful in gene therapy and for diagnosing or treating MTHFR deficiency
XX      which is associated with cardiovascular disorders or cancer
XX
XX      Claim 1; Fig 1A-F; 93pp; English.

The present sequence is that of cDNA coding for human
methylenetetrahydrofolate reductase (MTHFR, see AAY96186), an enzyme
catalysing the NADPH-linked reduction of 5,10-methylenetetrahydrofolate
to 5-methyltetrahydrofolate, a co-substrate for methylation of
homocysteine to methionine. To identify human MTHFR cDNA, PCR
primers based on the porcine sequence were used to screen a human
liver lambda-gt10 cDNA library by PCR. A 1266 bp fragment was
obtained, and this was used to screen a human colon carcinoma cDNA
library to obtain the 2.2 kb clone. The MTHFR gene (see AAAS0634)
maps to chromosome 1p36.6. A cDNA probe for human MTHFR, which
hybridises to the present sequence, is claimed. This probe can be
used to identify MTHFR sequence abnormalities in individuals with
severe or mild MTHFR deficiency. These abnormalities may comprise
a mutation selected from 167G to A, 482G to A, 559C to T, 677C to
T, 692C to T, 764C to T, 792+1G to A, 985C to T, 1015C to T, 1081C
to T, 1298A to C and 1317T to C. MTHFR deficiency may be associated
with a cardiovascular disorder, cancer (especially neuroblastoma or
colorectal carcinoma), osteoporosis, neural tube defect in an
offspring of a patient, neurological disorders, and other disorders
influenced by folic acid metabolism. Also claimed are methods for
treating MTHFR deficiency by gene therapy or by administration of
MTHFR protein. Cancer can be treated by inhibiting MTHFR gene
expression or MTHFR protein activity, or by administering an agent
that modifies MTHFR gene expression.

Sequence 2220 BP; 501 A; 658 C; 620 G; 441 T; 0 other:

Query Match 99.6%; Score 2186.6; DB 21; Length 2220;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 2189; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
Oy      1 aatccgagacatggtgacgaagccagcagaagaaacagcagcctaacctgtctggag 60
Db      1 aatccgagacatggtgacgaagccagcagaagaaacagcagcctaacctgtctggag 60
Oy      61 ggcagtcagcagcagtcgagagctccaaagatgctgagatgttccacccggagc 120

```

Db 61 ggcagtcgcaagcagtcgagtcgagagctccaaagatgctcgagatgttccaccccggtc 120
QY 121 ctggaccctctgagcagatgagagatccggagagagatgagcggcgaatttgaaatctgt 180
Db 121 ctggaccctctgagcagatgagagatccggagagagatgagcggcgaatttgaaatctgt 180
QY 181 gacaaagtgtctccctcgtgaaattctccctccgaaactgtctgagagagctgtcaatctc 240
Db 181 gacaaagtgtctccctcgtgaaattctccctccgaaactgtctgagagagctgtcaatctc 240
QY 241 atctcaaggtttgacggagatgacagcaggtgagccccctctacatgagctgtaacctgac 300
Db 241 atctcaaggtttgacggagatgagcagcaggtgagccccctctacatgagctgtaacctgac 300
QY 301 ccaagcaggtgacccctgtgctcagacaagagagacctctccatgatatgccaagacgcgc 360
Db 301 ccaagcaggtgacccctgtgctcagacaagagacctctccatgatatgccaagacgcgc 360
QY 361 gtgaaactctgtggtcttgagagacacacctctgacatgacctgtgctgcagcgccctgag 420
Db 361 gtgaaactctgtggtcttgagagacacacctctgacatgacctgtgctgcagcgccctgag 420
QY 421 gagatcacggcgccatctgcacaaagctaaagcagctggcgctgaggaacatactggcgctg 480
Db 421 gagatcacggcgccatctgcacaaagctaaagcagctggcgctgaggaacatactggcgctg 480
QY 481 cgggagagacccaatagtgagccaagtggagagagagagagagagagagagagagagagag 540
Db 481 cgggagagacccaatagtgagccaagtggagagagagagagagagagagagagagagagag 540
QY 541 gaccctgtgagagacacatccgaaagtgtggtctgtaactcttctgaaatctgtgtgcaagt 600
Db 541 gaccctgtgagagacacatccgaaagtgtggtctgtaactcttctgaaatctgtgtgcaagt 600
QY 601 taccccaagagccaccccggaagcagagagctttgagctgtgacctgtgaagcagctgaagag 660
Db 601 taccccaagagccaccccggaagcagagagctttgagctgtgacctgtgaagcagctgaagag 660
QY 661 aaggtgtgtgctggagccgagatctcatcagcagcagcttctcttgaagctgtgacacatctc 720
Db 661 aaggtgtgtgctggagccgagatctcatcagcagcagcttctcttgaagctgtgacacatctc 720
QY 721 ttcgcgtctgtgaaagcagtcagcagcagcagcagcagcagcagcagcagcagcagcagc 780
Db 721 ttcgcgtctgtgaaagcagtcagcagcagcagcagcagcagcagcagcagcagcagcagc 780
QY 781 tttcccatcagagctac 840
Db 781 tttcccatcagagctac 840
QY 841 ccaacagagagatcaaggagctgtatgagccaatcaaaagacagatgtgcatactccgcaac 900
Db 841 ccaacagagagatcaaggagctgtatgagccaatcaaaagacagatgtgcatactccgcaac 900
QY 901 tatgtgacatgagctgagcgtgtgagcgtgtgagcagagcttctgagagcttctgagagctg 960
Db 901 tatgtgacatgagctgagcgtgtgagcgtgtgagcagagcttctgagagcttctgagagctg 960
QY 961 ggcctccactcttaac 1020
Db 961 ggcctccactcttaac 1020
QY 1021 gggagatgtgagctgagagaccccgagctccctacacacacacacacacacacacacac 1080
Db 1021 gggagatgtgagctgagagaccccgagctccctacacacacacacacacacacacacac 1080
QY 1081 cgcgcagagagagatgtagctccatctctctggtctccagaccaaaggttaactctac 1140
Db 1081 cgcgcagagagagatgtagctccatctctctggtctccagaccaaaggttaactctac 1140
QY 1141 cgtaccacagagatgtagagagatcccttaacagcgctggggaattctctccctctgc 1200
Db 1141 cgtaccacagagatgtagagagatcccttaacagcgctggggaattctctccctctgc 1200

QY 1201 ttgaggagctgaaagacatactactcttctactctgaaagcagatgccccaagagagag 1260
Db 1201 ttgaggagctgaaagacatactactcttctactctgaaagcagatgccccaagagagag 1260
QY 1261 ctgtgaaagatgtgaggagagctgaaagcagatgaaagcagatgtcttgaagcttctgtc 1320
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QY 1321 cttaactctcggagagaccaaaccggatgtgtcaaaaagtgtactgtgctgtccctggaac 1380
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QY 1381 gatagacccctggagctgtgagacacagctctgagaaagagagctgtgctgctggaacgc 1440
Db 1381 gatagacccctggagctgtgagacacagctctgagaaagagagctgtgctgctggaacgc 1440
QY 1441 caggcatctcacaacacatactcacaagcccaacacacacacacacacacacacacacac 1500
Db 1441 caggcatctcacaacacatactcacaagcccaacacacacacacacacacacacacacac 1500
QY 1501 atcgtggctgtgggccccagcggggtatgtcttccagaagcttaataagattttc 1560
Db 1501 atcgtggctgtgggccccagcggggtatgtcttccagaagcttaataagattttc 1560
QY 1561 acttcccgagacagcggaaagcactctctgaaagtgtctgaaagatgacagctccgggt 1620
Db 1561 acttcccgagacagcggaaagcactctctgaaagtgtctgaaagatgacagctccgggt 1620
QY 1621 aattacaacacttgcataatgtgaaaggtgaaaaacatacacaatgcctctgaactgtgacgc 1680
Db 1621 aattacaacacttgcataatgtgaaaggtgaaaaacatacacaatgcctctgaactgtgacgc 1680
QY 1681 aatgtgtcactctgggagatcttccctgggagagatctcaccgacacagctgagat 1740
Db 1681 aatgtgtcactctgggagatcttccctgggagagatctcaccgacacagctgagat 1740
QY 1741 ccggtcagactcagttctgaaagcagagccttctgctgagatgtgagcgtgtgga 1800
Db 1741 ccggtcagactcagttctgaaagcagagccttctgctgagatgtgagcgtgtgga 1800
QY 1801 aagctgtatgagagagatccctcccgacacacacacacacacacacacacacacacacac 1860
Db 1801 aagctgtatgagagagatccctcccgacacacacacacacacacacacacacacacacac 1860
QY 1861 ttcctgtcacaacctgtgtgacaatgacttccactgtgacaactgtcctgtgaggtgtg 1920
Db 1861 ttcctgtcacaacctgtgtgacaatgacttccactgtgacaactgtcctgtgaggtgtg 1920
QY 1921 gaaagcaaatgtggagcttctcaaaagcaccacaggaatgtgaaagaaacggaggtcca 1980
Db 1921 gaaagcaaatgtggagcttctcaaaagcaccacaggaatgtgaaagaaacggaggtcca 1980
QY 1981 tgaactgtgtcctgacagcctctgtgtgagacacacacacacacacacacacacacacac 2040
Db 1981 tgaactgtgtcctgacagcctctgtgtgagacacacacacacacacacacacacacacac 2040
QY 2041 gtgcgtgtctcttgggaactccactctctgtgtcttctccacacacacacacacacacac 2100
Db 2041 gtgcgtgtctcttgggaactccactctctgtgtcttctccacacacacacacacacacac 2100
QY 2101 ccccaactgacaatgtgagctgagagctgagagcttccagagcttctccctgagagag 2160
Db 2101 ccccaactgacaatgtgagctgagagctgagagcttccagagcttctccctgagagag 2160
QY 2161 tcggcccaacatgagaaactagtaactctgtctca 2196
Db 2161 tcggcccaacatgagaaactagtaactctgtctca 2196

RESULT 3
AAD20462
ID AAD20462 standard; cDNA; 2220 BP.

Query Match	99.6%	Score 2186.6	DB 22	Length 2220
Best Local Similarity	99.7%	Pred. No. 0		
Matches 2189	Conservative	0	Mismatches 7	Indels 0
			Gaps	0
1	aattccgagcattgttgaacgaagccagagaggaacagcagctcaacccctgtgag	60		
1				
1	aattccgagcattgttgaacgaagccagagaggaacagcagctcaacccctgtgag	60		
61	ggcagctgccagcagctgagcagctgagcagctcccaagaatgctgagatgttccaccgggc	120		

Db	61	ggcagctgcacagctgagcagtgagagctccaaagatacttcagagatgttccacccgggc	120
Oy	121	cggagccctgagacgagacatgagagagctccggagagagatactgagcgagcttgaaatctgt	180
Db	121	cggagccctgagcagcatagagagagctccggagagagatactgagcgagcttgaaatctgt	180
Oy	181	gacaaagtgtctccctggaattctccctctcgaacagctgagaggagctgtcaatctc	240
Db	181	ggcaaaagtgtctccctggaattctccctctcgaacatctgtgagaggagctgtcaatctc	240
Oy	241	atctcaaaagtttgacacggatactgacagagctggccccctctacaataagcgtagacttgacac	300
Db	241	atctcaaaagtttgacacggatactgacagagctggccccctctacaataagcgtagacttgacac	300
Oy	301	ccaaagagttgacccctgctcagacaaaggagacatctctcatalgtatctgcagacacagcc	360
Db	301	ccaaagagttgacccctgctcagacaaaggagacatctctcatalgtatctgcagacacagcc	360
Oy	361	gtgaaactactgtgtgctctggagaaacatctctgtacatactgacccctgcgcgtcaagcctcgag	420
Db	361	gtgaaactactgtgtgctctggagaaacatctctgtacatactgacccctgcgcgtcaagcctcgag	420
Oy	421	ggaatcacagvggacatctgcacaaagctaaagacgcttgagcccttgagagacatcatctgagcctg	480
Db	421	ggaatcacagvggacatctgcacaaagctaaagacgcttgagcccttgagagacatcatctgagcctg	480
Oy	481	cggggagacccaatagtgtgacagctgggaaagagagagagagcttcaactacgacgtg	540
Db	481	cggggagacccaatagtgtgacagctgggaaagagagagagagagcttcaactacgacaggtg	540
Oy	541	gacccgtggagagacatctccgagctgagatttgggtgaaactcttgacatctgtgtggaggt	600
Db	541	gacccgtggagagacatctccgagctgagatttgggtgaaactcttgacatctgtgtggaggt	600
Oy	601	taccccaaaggccaccccgaaagcagaggagctcttgaggtctgacctgaaagcacttgaaaggag	660
Db	601	taccccaaaggccaccccgaaagcagaggagctcttgaggtctgacctgaaagcacttgaaaggag	660
Oy	661	aaggtgtttggggagacggattatcatatacagaggttttctttgaagcttgacaaatc	720
Db	661	aaggtgtttggggagacggattatcatatacagaggttttctttgaagcttgacaaatc	720
Oy	721	ttccgctttgaaagagcatgacacgaaatgtgacatctgacatctgccccatctgccccggatc	780
Db	721	ttccgctttgaaagagcatgacacgaaatgtgacatctgacatctgccccatctgccccggatc	780
Oy	781	tttcccatccagggctacacatctcccttcggacagctctgtgaagctgtctcaagcttgagagtg	840
Db	781	tttcccatccagggctacacatctcccttcggacagctctgtgtgaagctgtctcaagcttgagagtg	840
Oy	841	ccaaagagatcacagagagctgatatgagacccaatacaaaagacaacagatgctgcacatccgacac	900
Db	841	ccaaagagatcacagagagctgatatgagacccaatacaaaagacaacagatgctgcacatccgacac	900
Oy	901	tatggcatcgagctgcgcgtgagcctgtgccaaggagctcttgccaagtgtgctgtgtgcca	960
Db	901	tatggcatcgagctgcgcgtgagcctgtgccaaggagctcttgccaagtgtgctgtgtgcca	960
Oy	961	ggccctcaactctacaacccctcaaacgcggagatgtgctacacaaagatgtctgtgaagcgctgt	1020
Db	961	ggccctcaactctcaacccctcaaacgcggagatgtgctacacaaagatgtctgtgaagcgctgt	1020
Oy	1021	ggagatgtgacttgagacccccaagcgctctccataccttgagctctcaagtgtccaccccaag	1080
Db	1021	ggagatgtgacttgagacccccaagcgctctccataccttgagctctcaagtgtccaccccaag	1080
Oy	1081	cgcgcgagagagatgtgacgttccatctctcttgagctccagagcaaaaggttatcatctac	1140
Db	1081	cgcgcgagagagatgtgacgttccatctctcttgagctccagagcaaaaggttatcatctac	1140
Oy	1141	cgtacccagaggtgagacaggttccctaaagcgcgcttgaggcaattccctctccctctgc	1200

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Db 1141 cgtaccaggagtggaacgaagttccctaacgagcgtggtggcaattcctctccctgccc 1200
QY 1201 ttctggagagctgaagactactactactctcttactctgaagaagcccccaaggagagag 1260
Db 1201 ttctggagagctgaagactactactactctcttactctgaagaagcccccaaggagagag 1260
QY 1261 ctgtctaaagatctgggggggagagcgtgancagatgaagcgaagctctttnaagcttctgt 1320
Db 1261 ctgtctaaagatctgggggggagagcgtgancagatgaagcgaagctctttnaagcttctgt 1320
QY 1321 ctctactctctcgagaaacaaacacggaatggtcacaaagtgtactgtccctgtgaaac 1380
Db 1321 ctctactctctcgagaaacaaacacggaatggtcacaaagtgtactgtccctgtgaaac 1380
QY 1381 gatgagccctcgagcgtgagcagcagcctgtctgaagagagagctgtgtgggtgaaacgc 1440
Db 1381 gatgagccctcgagcgtgagcagcagcctgtctgaagagagagctgtgtgggtgaaacgc 1440
QY 1441 caggagcattccctcaactcaactcaacagcccaatcaacagcggaagcgtctcccgacccc 1500
Db 1441 caggagcattccctcaactcaactcaacagcccaatcaacagcggaagcgtctcccgacccc 1500
QY 1501 atcgttggtctgggccccagcggggtatgtcttccagaaggcctaactagaagtttttc 1560
Db 1501 atcgttggtctgggccccagcggggtatgtcttccagaaggcctaactagaagtttttc 1560
QY 1561 actcccgcgagacagcgagacactctgtcaagtgtctgaagaagtacagagctccgggtt 1620
Db 1561 actcccgcgagacagcgagacactctgtcaagtgtctgaagaagtacagagctccgggtt 1620
QY 1621 aattaccacttgtcaatgtgaagggttgaacaatcaacaaatgccttgaaactgtacgcg 1680
Db 1621 aattaccacttgtcaatgtgaagggttgaacaatcaacaaatgccttgaaactgtacgcg 1680
QY 1681 aatgctgtcaacttgaggcactctccctggcgagagatcatccagcccgacagtgatgat 1740
Db 1681 aatgctgtcaacttgaggcactctccctggcgagagatcatccagcccgacagtgatgat 1740
QY 1741 cccgtcagctcatgtctctggaagagcagagccttgcctgtagattgagcggtggga 1800
Db 1741 cccgtcagctcatgtctctggaagagcagagccttgcctgtagattgagcggtggga 1800
QY 1801 aagctgtatgagagagaggtcccgctcccgacacatcatcaatgatacatccagcaactac 1860
Db 1801 aagctgtatgagagagaggtcccgctcccgacacatcatcaatgatacatccagcaactac 1860
QY 1861 ttccctgtcaacactgtgtgacaatgacttcccaactgtgacaactgtcctgtgacagtggtg 1920
Db 1861 ttccctgtcaacactgtgtgacaatgacttcccaactgtgacaactgtcctgtgacagtggtg 1920
QY 1921 gaagaacacatttgagacttctcaacagcccaacccagaatgcgagagaaacgagagctcca 1980
Db 1921 gaagaacacatttgagacttctcaacagcccaacccagaatgcgagagaaacgagagctcca 1980
QY 1981 tgaccctcgctcctgaagcctctgctgtgagccactcctctcccgacttccctcctccaca 2040
Db 1981 tgaccctcgctcctgaagcctctgctgtgagccactcctctcccgacttccctcctccaca 2040
QY 2041 gtgtctgtctctcttggaactcaactcctctctgtctctcccaaccccgagctccaactc 2100
Db 2041 gtgtctgtctctcttggaactcaactcctctctgtctctcccaaccccgagctccaactc 2100
QY 2101 ccccaactgtacaatgagcagctagaactgagatggaagcttccagagcttctcttgagactgag 2160
Db 2101 ccccaactgtacaatgagcagctagaactgagatggaagcttccagagcttctcttgagactgag 2160
QY 2161 tcggcccaacatgggaacctagactctctgtcctta 2196
Db 2161 tcggcccaacatgggaacctagactctctgtcctta 2196

```

RESULT 4
AAT09689

```

ID AAT09689 standard; cDNA: 2219 BP.
AC AAT09689;
XX
XX
XX 15-OCT-1996 (first entry)
DT
XX
XX Human methylene-tetrahydrofolate-reductase cDNA.
DE
XX
XX Methylene-tetrahydrofolate-reductase; MTHFR; gene therapy;
KM cardiovascular disease; neurological disease; folic acid metabolism;
KW EC-1.5.1.20; enzyme; ss.
XX
XX Homo sapiens.
OS
XX
XX
XX Key Location/Qualifiers
XX CDS 13..1980
XX FT /tag= a
XX
XX
XX W09533054-A1.
XX
XX 07-DEC-1995.
XX
XX
XX 25-MAY-1995; 95MO-CA00314.
XX
XX 26-MAY-1994; 94GB-0010620.
XX
XX (UVMC-) UNIV MCGILL.
XX
XX Goyette P, Rozen R;
XX
XX WPI: 1996-030565/03.
XX
XX P-PSDB: AAR8358.
XX
XX Human methylene-tetrahydrofolate reductase cDNA probe - for
XX detection of sequence abnormalities in methylene-tetrahydrofolate
XX reductase e.g. in cardiovascular, neurological or folic acid
XX metabolism disorders
XX
XX PS Disclosure: Fig. 6A-6C; 66pp; English.
XX
XX
XX This sequence encoding human MTHFR has been localised to chromosome
XX 1p36.3. It may be used for the construction of DNA probes which may
XX be used for the identification of sequence abnormalities in patients
XX CC with severe or mild MTHFR deficiency. The resulting probe may also
XX CC be used in gene therapy to produce the MTHFR protein.
XX
XX
XX Sequence 2219 BP; 501 A; 656 C; 620 G; 442 T; 0 other;
SQ

```

Query Match 99.5%; Score 2185; DB 17; Length 2219;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 2188; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

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Db 1 aattccggagcattgttgaacgaagccagaaggaacagagctcaacccctgtgtgag 60
QY 61 ggcagtgacagcagctgagcagtgagagctccaagaatgattgagatggttccaccccgagc 120
Db 61 ggcagtgacagcagctgagcagtgagagctccaagaatgattgagatggttccaccccgagc 120
QY 121 ctggaacctgagcagcagatagagaccccggaagaatgagagcgagatggaatctggt 180
Db 121 ctggaacctgagcagcagatagagaccccggaagaatgagagcgagatggaatctggt 180
QY 181 gacaagtgttctccctgtgaattctccctcctcgaaactgtcgaagtgagtgatcaatctc 240
Db 181 gacaagtgttctccctgtgaattctccctcctcgaaactgtcgaagtgagtgatcaatctc 240
QY 241 atctcaaggtttgacccggatgagcaggttgagccctcctacaataacgtgacccggagac 300
Db 241 atctcaaggtttgacccggatgagcaggttgagccctcctacaataacgtgacccggagac 300

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QY 301 ccagcagctgacccctgctcagacgaagacccctccatgatagtatcgcacagaccgc 360
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Db 301 ccagcagctgacccctgctcagacgaagacccctccatgatagtatcgcacagaccgc 360
QY 361 gtgaactactgtgacctgagagacacatccctgcacatagtacctgtcgcgttaagcgctggag 420
|||||
Db 361 gtgaactactgtgacctgagagacacatccctgcacatagtacctgtcgcgttaagcgctggag 420
QY 421 gaatacagcgacatctgcacaaagctaaagcagctgagccctgaggaacatcatgagcgctg 480
|||||
Db 421 gaatacagcgacatctgcacaaagctaaagcagctgagccctgaggaacatcatgagcgctg 480
QY 481 cgggagagaccacaaatagtgagaccaaagtggaaagaggaugaaagagcttcaactacgcaagt 540
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Db 481 cgggagagaccacaaatagtgagaccaaagtggaaagaggaugaaagagcttcaactacgcaagt 540
QY 541 gacctgtgtagagacacatcgaagatgagttgtgtagacttgaacttgaactctgtgtagcgagt 600
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Db 541 gacctgtgtagagacacatcgaagatgagttgtgtagacttgaacttgaactctgtgtagcgagt 600
QY 601 taccccaagagcaccgccgaagcagggagcttgaagcttgacctgaagcacttgaagagag 660
|||||
Db 601 taccccaagagcaccgccgaagcagggagcttgaagcttgacctgaagcacttgaagagag 660
QY 661 aaggtgtatcgaggagccgattccatcatcagcagcttcttttgaagcttgacacatc 720
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Db 661 aaggtgtatcgaggagccgattccatcatcagcagcttcttttgaagcttgacacatc 720
QY 721 ttcgcgtttgtagagcatcagacgaatgagcatcacttgcaccatcgcgcccgagatc 780
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Db 721 ttcgcgtttgtagagcatcagacgaatgagcatcacttgcaccatcgcgcccgagatc 780
QY 781 ttcccatcagaggtacacatccctcctgcgcagcttgtagagctgtgccaaagctggagagt 840
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Db 781 ttcccatcagaggtacacatccctcctgcgcagcttgtagagctgtgccaaagctggagagt 840
QY 841 ccacaaagagatcagagcagtgatgtagcacaatacgaacaaagacgaatgtgcacatccgacac 900
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Db 841 ccacaaagagatcagagcagtgatgtagcacaatacgaacaaagacgaatgtgcacatccgacac 900
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QY 1081 cgcggagagagagatgtacgtcccatcttctggcctccagacaaagaggttatactaac 1140
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QY 1261 ctgctgaagatgttgaggagagagctgancagtgaaacaaatgtcttgtagagcttttgtt 1320
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QY 1321 cttaactctcggagaaaccaaaccgaatgtgtacaaagtgaacttgcctgccttgagac 1380
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Db 1321 cttaactctcggagaaaccaaaccgaatgtgtgtacaaagtgaacttgcctgccttgagac 1380
QY 1381 gatagacccctgagcgtgtagaacagcagctgtgtagaagagagcgtgaggtgtagaacgc 1440
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Db 1381 gatagacccctgagcgtgtagaacagcagctgtgtagaagagagctgtgaggtgtagaacgc 1440
QY 1441 caggtcatcctcaacatcacaactcagccagcccaaatcaacggagagcgtccctccgacccc 1500
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Db 1441 caggtcatcctcaacatcacaactcagccagcccaaatcaacggagagcgtccctccgacccc 1500
QY 1501 atcgtgagctgggcccagcaggggtatgtctccagaagggcctaactaagatttttc 1560
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Db 1501 atcgtgagctgggcccagcaggggtatgtctccagaagggcctaactaagatttttc 1560
QY 1561 acttcccgagagacagcaggaagcacttctgcgaagtgtcgaagaagtacagactccgagct 1620
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Db 1561 acttcccgagagacagcaggaagcacttctgcgaagtgtcgaagaagtacagactccgagct 1620
QY 1621 aattacacacttgcataatgtgaagggtgaaatacacaacaaatgcccctgaactgacgcg 1680
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Db 1621 aattacacacttgcataatgtgaagggtgaaatacacaacaaatgcccctgaactgacgcg 1680
QY 1681 aatgtctcaacttggggcacttccctggcgagagatcatccagaccagtagtggat 1740
|||||
Db 1681 aatgtctcaacttggggcacttccctggcgagagatcatccagaccagtagtggat 1740
QY 1741 cccgtcagcttcaatgtctcgtgaagagacgagccttgcctgtagatltgagcgttggga 1800
|||||
Db 1741 cccgtcagcttcaatgtctcgtgaagagacgagccttgcctgtagatltgagcgttggga 1800
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|||||
Db 1801 aagctgtatgagagagatcccgctccgcacacatcatccagtaactcatccagacacatc 1860
QY 1861 ttccgtgtcaacctgtgtgacaatgacttccactgagacactgacctgtgcagctgtgtg 1920
|||||
Db 1861 ttccgtgtcaacctgtgtgacaatgacttccactgagacactgacctgtgcagctgtgtg 1920
QY 1921 gaagacacatltgagacttctcaacagccacccaagaatgagagagaaacgagctcca 1980
|||||
Db 1921 gaagacacatltgagacttctcaacagccacccaagaatgagagagaaacgagctcca 1980
QY 1981 tgacccgtgctctgagacgacctgtgtgagagacacttcttccggcttctcctccaca 2040
|||||
Db 1981 tgacccgtgctctgagacgacctgtgtgagagacacttcttccggcttctcctccaca 2040
QY 2041 gtgctgtctcttctggaactcacaactcctctcgtgtctctccaccccgactcactc 2100
|||||
Db 2041 gtgctgtctcttctggaactcacaactcctctcgtgtctctccaccccgactcactc 2100
QY 2101 ccccaactgacaatgagcagctagatgtgaggttccaggtcttctctgagacctggag 2160
|||||
Db 2101 ccccaactgacaatgagcagctagatgtgaggttccaggtcttctctgagacctggag 2160
QY 2161 tcggcccaactgggaactagtaactctgtctta 2196
|||||
Db 2161 tcggcccaactgggaactagtaactctgtctta 2196

RESULT 5
AAT09694
ID AAT09694 standard; cDNA; 2220 BP.
AC AAT09694;
AC 15-OCN-1996 (first entry)
DE Human methylene-tetrahydrofolate-reductase cDNA.
XX
XX
XX Methylenetetrahydrofolate-reductase; MTHFR; gene therapy;
KW cardiovascular disease; neurological disease; folic acid metabolism;
KW EC-1.5.1.20; enzyme; ss.
OS Homo sapiens.
XX
XX
FH Key Location/Qualifiers

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FI mat_peptide 1..1980
FI /*tag= a
XX WO9533054-A1.
XX
XX 07-DEC-1995.
XX
XX 25-MAY-1995; 95WO-CA00314.
XX
XX 26-MAY-1994; 94GB-0010620.
XX
XX (UYMC-) UNITV MCGILL.
XX
XX Goyette P, Rozen R;
XX
XX WPI: 1996-030565/03.
XX
XX P-PSDB: AAT09694.
XX
XX Human methylene:tetra:hydro:folate reductase cDNA probe - for
XX detection of sequence abnormalities in methylene:tetra:hydro:folate
XX reductase e.g. in cardiovascular, neurological or follic acid
XX metabolism disorders
XX
XX PS Disclosure; Fig.1A-1F; 66pp; English.
XX
XX This sequence encoding human MTHFR has been localised to chromosome
XX 1p36.3. It may be used for the construction of DNA probes which may
XX be used for the identification of sequence abnormalities in patients
XX with severe or mild MTHFR deficiency. The resulting probe may also
XX be used in gene therapy to produce the MTHFR protein.
XX
XX SO Sequence 2220 BP; 501 A; 657 C; 620 G; 442 T; 0 other:

Query Match 99.5%; Score 2185; DB 17; Length 2220;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 2188; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 1 aattccggaacccatgtggaacgaagccagaggaacagacagctcaacccctgttgag 60
DB 1 aattccggaacccatgtggaacgaagccagaggaacagacagctcaacccctgttgag 60
QY 61 ggcagtgccagcagtgagcagtgagagctccaagaatagttcgaagatgttccacccgggc 120
DB 61 ggcagtgccagcagtgagcagtgagagctccaagaatagttcgaagatgttccacccgggc 120
QY 121 ctggaccctgaagcgagctgagagactccggagagaagatgagcgagctggaactcgtgt 180
DB 121 ctggaccctgaagcgagctgagagactccggagagaagatgagcgagctggaactcgtgt 180
QY 181 gacaaagtgtctccctcggaattctccctcctcgaaactgtgagggagctgtcaatctc 240
DB 181 gacaaagtgtctccctcggaattctccctcctcgaaactgtgagggagctgtcaatctc 240
QY 241 atctcaaggtttgacccgagatgagcagagtggtgcccctcaacatagcgtgactgtgac 300
DB 241 atctcaaggtttgacccgagatgagcagagtggtgcccctcaacatagcgtgactgtgac 300
QY 241 atctcaaggtttgacccgagatgagcagagtggtgcccctcaacatagcgtgactgtgac 300
DB 241 atctcaaggtttgacccgagatgagcagagtggtgcccctcaacatagcgtgactgtgac 300
QY 301 ccaagcaggtgacccctggtctcagacaagagaaactcctcctcatgatatcgccagaccgc 360
DB 301 ccaagcaggtgacccctggtctcagacaagagaaactcctcctcatgatatcgccagaccgc 360
QY 361 gtgaactactgtgctcgagacacatccctcgaatgacactgtcgctcagcgccctgag 420
DB 361 gtgaactactgtgctcgagacacatccctcgaatgacactgtcgctcagcgccctgag 420
QY 421 gagatccgggacacatcccgacaagaagctaaagcagctgggcttgaggaacatcatgcgctg 480
DB 421 gagatccgggacacatcccgacaagaagctaaagcagctgggcttgaggaacatcatgcgctg 480
QY 481 cgggagagaccacaataggtgacacagtgaggagagagagagaggttcaactacgacgtg 540
DB 481 cgggagagaccacaataggtgacacagtgaggagagagagagaggttcaactacgacgtg 540

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QY 541 gacctgtgtaagcacatccgaagtgagttgtgtgactacttgacatctgtgtgagcagt 600
DB 541 gacctgtgtaagcacatccgaagtgagttgtgtgactacttgacatctgtgtgagcagt 600
QY 601 taaccccaaaagccaccccggaagcagggagctttgaggtcgactctgaagcaacttgaaagag 660
DB 601 taaccccaaaagccaccccggaagcagggagctttgaggtcgactctgaagcaacttgaaagag 660
QY 661 aaggtgtntcgagagcgacttccatcacaagcagctttctcttgaggctgacacatc 720
DB 661 aaggtgtntcgagagcgacttccatcacaagcagctttctcttgaggctgacacatc 720
QY 721 ttcgcgttctgtgaagcagatgacacgacatgagcacttgcacatgctcccgaggag 780
DB 721 ttcgcgttctgtgaagcagatgacacgacatgagcacttgcacatgctcccgaggag 780
QY 781 ttcccatccaggggtacacatccctctcgacagctgtgaagctgtccaaagctgagagtg 840
DB 781 ttcccatccaggggtacacatccctctcgacagctgtgaagctgtccaaagctgagagtg 840
QY 841 ccacagagatcaagagcgtgattgagccaatcaagaacacagatgctgcacatccgcaac 900
DB 841 ccacagagatcaagagcgtgattgagccaatcaagaacacagatgctgcacatccgcaac 900
QY 901 tatgcatcgagctgagcgtgagacgtgtccagagacctctgacagctgtgctgtgca 960
DB 901 tatgcatcgagctgagcgtgagacgtgtccagagacctctgacagctgtgctgtgca 960
QY 961 ggcctccactctacacccctcaacccgagatgtgtaccacagaggtgtgaaagcgctg 1020
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QY 1081 cgcagagaggaagatgatactgacatctctctgagcctcagacccaagaagttacatctac 1140
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QY 1141 cgtacccaagagatgaggacagatctccctaaacgagcgctggggcaatctccctctgac 1200
DB 1141 cgtacccaagagatgaggacagatctccctaaacgagcgctggggcaatctccctctgac 1200
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DB 1201 ttctgggagcttgagagactactactctctacacttgaaagagcagctccccaagagagag 1260
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QY 1381 gatgagcccttgacgagctgagacacagctgtcgaagagagagctgtcggtgtgaacgcg 1440
DB 1381 gatgagcccttgacgagctgagacacagctgtcgaagagagagctgtcggtgtgaacgcg 1440
QY 1441 caaggacatctcaccatcaactcaacagccacaacatacaacggagagagcgctccctcgaccc 1500
DB 1441 caaggacatctcaccatcaactcaacagccacaacatacaacggagagagcgctccctcgaccc 1500
QY 1501 atcgtgtgctgggcccacagcggggtatagtcttccagaagagcctactaagattttc 1560
DB 1501 atcgtgtgctgggcccacagcggggtatagtcttccagaagagcctactaagattttc 1560
QY 1561 acttcccgagagacagcggaacacatctcgaagtgtctgaagagatagcagctccgggt 1620
DB 1561 acttcccgagagacagcggaacacatctcgaagtgtctgaagagatagcagctccgggt 1620

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OY 1621 aattaccactgtcaatgtaaggtgtaaaacatcaccaatgccctgaatgcagcg 1680
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 DB 1621 aattaccactgtcaatgtaaggtgtaaaacatcaccaatgccctgaatgcagcg 1680
 OY 1681 aatgctgtaacttggggacatctccctggcgagagatcatccagccacagtgatgat 1740
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 DB 1681 aatgctgtaacttggggacatctccctggcgagagatcatccagccacagtgatgat 1740
 OY 1741 cccgtcagcttcatgtctctggaagagagagccttggccctgtgaattgagcggtggga 1800
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 DB 1741 cccgtcagcttcatgtctctggaagagagagccttggccctgtgaattgagcggtggga 1800
 OY 1801 aagctgtatgagggagaggtcccccgtcccgacacatcatccagatcaccaagaactac 1860
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 DB 1801 aagctgtatgagggagaggtcccccgtcccgacacatcatccagatcaccaagaactac 1860
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 DB 1861 ttccctgtcaacccgtgtgtaaatgacttcccaatggaacatgtcctctggcaaggtggtg 1920
 OY 1921 gaagacacatgtggagcttctcaagaagccacccaagaatgagagaagaaagagcttcca 1980
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 DB 1921 gaagacacatgtggagcttctcaagaagccacccaagaatgagagaagaaagagcttcca 1980
 OY 1981 tgaacctgtctcagcagcctgtgtagagcaatcctctgtccgaccttccctccaca 2040
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 DB 1981 tgaacctgtctcagcagcctgtgtagagcaatcctctgtccgaccttccctccaca 2040
 OY 2041 gtgtcgtcttctctgggaactcccaatcctctgtgtctctccaccccgccctcccaatc 2100
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 DB 2041 gtgtcgtcttctctgggaactcccaatcctctgtgtctctccaccccgccctcccaatc 2100
 OY 2101 ccccaactgacaatgagcagctagactgtagtgaaggtcttccaggtcttctctgagactgag 2160
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 DB 2101 ccccaactgacaatgagcagctagactgtagtgaaggtcttccaggtcttctctgagactgag 2160
 OY 2161 tcggccccacatgggaactagtaactctctgctca 2196
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 DB 2161 tcggccccacatgggaactagtaactctctgctca 2196

 RESULT 6
 AAC91206
 ID AAC91206 standard: DNA; 2187 BP.
 XX
 AC AAC91206;
 XX
 DT 20-MAR-2001 (first entry)
 XX
 DE Human methylenetetrahydrofolate reductase gene SEQ ID NO: 1.
 XX
 KW Human; schizophrenia; developmental disorder; spina bifida cystica;
 KW Tourette's syndrome; bipolar illness; autism; conduct disorder;
 KW attention deficit disorder; obsessive compulsive disorder;
 KW chronic multiple tic syndrome; learning disorder; polymorphism; ds.
 XX
 OS Homo sapiens.
 XX
 PN WO200071754-A1.
 PD 30-NOV-2000.
 XX
 PF 24-MAY-2000; 2000WO-US14354.
 XX
 PR 25-MAY-1999; 99US-0318448.
 XX
 PA (UYNE-) UNIV NEW JERSEY MEDICINE & DENTISTRY.
 XX
 PI Johnson WG, Stenroos ES;
 XX
 DR WPI; 2001-025174/03.
 XX
 PT Diagnosing a developmental disorder, e.g. schizophrenia, by forming

PT datasets (DS) of genetic (e.g. genotypes of folate metabolism alleles)
 CC and environmental variables affecting an individual and then comparing
 PT these DS with reference DS -
 PS Disclosure; Page 114-115; 156pp; English.
 XX

The present invention provides a novel method of estimating the
 CC susceptibility of an individual to a developmental disorder using genetic
 CC and environmental variables. The method can be used in the diagnosis,
 CC prevention and treatment of disorders such as schizophrenia, spina bifida
 CC cystica, Tourette's syndrome, bipolar illness, autism, conduct disorders,
 CC attention deficit disorder, obsessive compulsive disorder, chronic
 CC multiple tic syndrome and learning disorders such as dyslexia.
 XX

Sequence 2187 BP; 479 A; 655 C; 616 G; 437 T; 0 other;

Query Match 99.78; Score 2177.6; DB 22; Length 2187;
 Best Local Similarity 99.78; Pred. No. 0;
 Matches 2180; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

OY 10 gccatgtgacaagcagaagcagaagaaacagacgctcaacccctgtgtgagggcagtgcc 69
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 DB 1 gccatgtgacaagcagaagcagaagaaacagacgctcaacccctgtgtgagggcagtgcc 60
 OY 70 agcagtgagcagtgagagctcccaagatagttgagatgttccaccccgagcctgagacct 129
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 DB 61 agcagtgagcagtgagagctcccaagatagttgagatgttccaccccgagcctgagacct 120
 OY 130 gaggcgatgagagaccccgagagaaatgagcgcgagatgtgaatctgtgtgacaagtgg 189
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 DB 121 gaggcgatgagagaccccgagagaaatgagcgcgagatgtgaatctgtgtgacaagtgg 180
 OY 190 ttctccctggaattcttccctccctcagactgtgagggagctgtcaatccatctcaagg 249
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 DB 181 ttctccctggaattcttccctccctcagactgtgagggagctgtcaatccatctcaagg 240
 OY 250 tttagccgagatggcagcaggtgtgcccctctacataagcgttgacacttggcaccagcaggt 309
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 OY 310 gaccctgtcacaagaagagacctctctcatgatatgcacagacagcgctggaactac 369
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 DB 301 gaccctgtcacaagaagagacctctctcatgatatgcacagacagcgctggaactac 360
 OY 370 tgtgacctgagacacatctcagatgacactgtgcctgacgagcgctggaagatcacg 429
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 DB 361 tgtgacctgagacacatctcagatgacactgtgcctgacgagcgctggaagatcacg 420
 OY 430 ggcacatgcacaagaagcagctgagcctgaggaacatcatgctgcgtgcggggagac 489
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 DB 421 ggcacatgcacaagaagcagctgagcctgaggaacatcatgctgcgtgcggggagac 480
 OY 490 ccaatagtgcccaatgaggaag 549
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 DB 481 ccaatagtgcccaatgaggaagagagagagagagagagagagagagagagagagagag 540
 OY 550 aagcacatccgaagtgagtttgtagtaactttagacatctgtgtgcaaggttaccccaaa 609
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 DB 541 aagcacatccgaagtgagtttgtagtaactttagacatctgtgtgcaaggttaccccaaa 600
 OY 610 ggcacccccgaag 669
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 DB 601 ggcacccccgaag 660
 OY 670 gcgagagccgagattcatcatcacgacagcttcttcttgagagctgacaacttccgcttt 729
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 DB 661 gcgagagccgagattcatcatcacgacagcttcttcttgagagctgacaacttccgcttt 720
 OY 730 gtgaagagcatgcacagagatgtggtacatctggccccatcgtcccgagatcttcccatc 789
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 DB 721 gtgaagagcatgcacagagatgtggtacatctggccccatcgtcccgagatcttcccatc 780

CC	offspring of a patient, neurological disorders, and other disorders
CC	influenced by folic acid metabolism. Also claimed are methods for
CC	treating MTHFR deficiency by gene therapy or by administration of
CC	MTHFR protein. Cancer can be treated by inhibiting MTHFR gene
CC	expression or MTHFR protein activity, or by administering an agent
CC	that modifies MTHFR gene expression. Isolation of the human MTHFR
CC	gene forms part of an effort to study MTHFR deficiency in
CC	homocystinuria and in multifactorial diseases.
SQ	Sequence 3283 BP; 664 A; 1001 C; 951 G; 667 T; 0 other;
Query Match	49.6%; Score 1089, 6; DB 21; Length 3283;
Best Local Similarity	68.6%; Pred. No. 3e-243;
Matches 2181; Conservative	0; Mismatches 7; Indels 989; Gaps 10;
OY	9 agacatgtgtaacgaagaccagaagaaacaacagacctcaaccctcttgtagggcagatgc 68
DB	57 agccatggtggaacgaagcacagaggaaacacagacctcaaccctcttgtagggcagtgc 116
OY	69 cagcagttgcagtgaagagtcctccaagaatgttgcagatatgtccaaccccgsgctgagacc 128
DB	117 cagcagttgcagtgagagagctcccaagaatgttgcagatatgtccaaccccgsgctgagacc 176
OY	129 tgcgcgcactgaagagcatcccgaggagagatagtgagccgatgtggaattcgtgtgacaagt 188
DB	177 tgcgcgcactgagagagcatcccgaggagagatagtgagccgatgtggaattcgtgtgacaagt 236
OY	189 gtctccctcggaaattcttcctccctctggaactgcttgaggagagctgtcaatctca-- 246
DB	237 gtctccctcggaaattcttcctccctctggaactgcttgaggagagctgtcaatctca-- 296
OY	247 ----- 246
DB	297 gtaaatcatgcaagtttaagtgtagagagcgggagtgtagctctcggagacgaatgtga 356
OY	247 ----- aggttgaccggatgtgcagcag 268
DB	357 ttctctctggaacatctctcttcaagaaaacccccctacagallcttgacccgagatgcagcag 416
OY	269 gtggccccccttaacatagacgtgaacctgagccacagcagatgtgacccctgtgacaaag 328
DB	417 gtggccccccttaacatagacgtgaacctgagccacagcagatgtgacccctgtgacaaag 476
OY	329 agacctctccatgatgatgtatcgcagacacgcgcgtgaaactactgtgacctgtgaaacatcc 388
DB	477 agacctctccatgatgatgtatcgcagacacgcgcgtgaaactactgtgacctgtgaaacatcc 536
OY	389 tgacacatgaaactgtgtgcctgcacagagcctctgtagagagatcaacagcgscactctcacaaagcta 448
DB	537 tgacacatgaaactgtgtgcctgcacagagcctctgtagagagatcaacagcgscactctcacaaagcta 596
OY	449 agcagctgagcctgtgaggaacaatacattgagcgtctcggg----- 485
DB	597 agcagctgagcctgtgaggaacaatacattgagcgtctcggg----- 656
OY	486 ----- 485
DB	657 acactctgggtctctgcgtcttccgcggaagcctctgtaggttggtgtgagaccgaatgataatg 716
OY	486 ----- agaccacaataggtgacccagtgtggaagagagggauagagagcttc 528
DB	717 acctccacaacacccctgcagaccaccaaataaggtgtgaccaaggtggaagagagggauagagcttc 776
OY	529 aactacgcagtgagcctcgtgtgaagcacacatccggaagtgaatttgttgactacttgaacatc 588
DB	777 aactacgcagtgagcctcgtgtgaagcacacatccggaagtgaatttgttgactacttgaacatc 836
OY	589 tttg----- 592
DB	837 tgtgtgagcaggtgagtggtgcctgcatcatcctgtgtgcsaggatgagctlaaggagagctgcac 896
OY	593 -----tgacaggtttaccccaaa 609

Db	897	cttgaacaggtgvgagccagcctctcttgacttcaatccctattgycaggttaccaccaa		956
Qy	610	ggccaccgccgaagcagggagcttttgaagcttgagacttgagacattgaaaggaaggtgtnt		669
Db	957	ggccaccgccgaagcagggagcttttgaagcttgagacttgagacattgaaaggaaggtgtnt		1016
Qy	670	ggcggaagccgatttcatcatcaacgaacttttttgaagcttgaacatcttcggctt		729
Db	1017	ggcggaagccgatttcatcatcaacgaacttttttgaagcttgaacatcttcggctt		1076
Qy	730	gtcaagagcatlgaacccgaatggtgcatcttgcgcacatgcgtcccggaattctccatc		789
Db	1077	gtcaagagcatlgaacccgaatggtgcatcttgcgcacatgcgtcccggaattctccatc		1136
Qy	790	-----	-----	789
Db	1137	caagtgaggggcccagagagaccataagcttccctccaccccatctcaacgcgtctggcc		1196
Qy	790	-----	caagtgataccatccctctggagactttg	819
Db	1197	agcagccgcacacagccctcaatgtctctggacagaggtctaccatccctcttggagcttgg		1255
Qy	820	aagctgtccaaagctgvgaggtgcccagagagatcaaaagacgttgattgaagccaataaagac		879
Db	1257	aagctgtccaaagctgvgaggtgcccagagagatcaaaagacgttgattgaagccaataaagac		1318
Qy	880	aacgaatgtctccatcccgcaactatgcatgacgtggccgttgagcccttggccagagactt		939
Db	1317	aacgaatgtctccatcccgcaactatgcatgacgtggccgttgagcccttggccagagactt		1376
Qy	940	ctggccagtggtcttgggtgcccagccctccactcttacaacctcaaccgcggaatgtgtacc		999
Db	1377	ctggccagtggtcttgggtgcccagccctccactcttacaacctcaaccgcggaatgtgtacc		1436
Qy	1000	acagaggtgctcgaaagccgcttgggaatgttgacgtgaagac-----		1038
Db	1437	acagaggtgctcgaaagccgcttgggaatgttgacgtgaagac-----		1496
Qy	1039	-----	-----	1038
Db	1497	agagatcccccagagagaggttccaaagacagccctccctctagccaatcccttgtctcaa		1556
Qy	1039	-----	cccaagcgttcccttacccttggtctcaatgtgcccacccaa	1079
Db	1557	ttctctgtcccatcctcaacccagcgttccctccatcccttggctctcaatgtgcccacccaa		1616
Qy	1080	ggccgcagagaaagatgtatagcttccatcttctgggctccaaacaaagatatacatla		1139
Db	1617	ggccgcagagaaagatgtatagcttccatcttctgggctccaaacaaagatatacatla		1676
Qy	1140	ccgtacccagagatgvggaacgaatctccctaaagccgct-----		1177
Db	1677	ccgtacccagagatgvggaacgaatctccctaaagccgctcttgaaggtcctgcagaccttcc		1736
Qy	1178	-----	-----	1177
Db	1737	ttgcaataacatcttttcttcttggagcgagctccctctgtcaagagatgtgcccgtgacct		1796
Qy	1178	-----	ggggcaatctctctcccttgccttggggagcttgaagagact	1219
Db	1797	ctggacacccctctgcgcaggggcgaatctcttcccttgccttggggagcttgaagagact		1856
Qy	1220	actaccccttctacttgaagaagcaagtcccccagaagagagctctctgaagatgtvgggg		1279
Db	1857	actaccccttctacttgaagaagcaagtcccccagaagagagctctctgaagatgtvgggg		1916
Qy	1280	agagactgtanacagtgaagcagatgctcttgaagcttcttcttactctccggagaaac		1339
Db	1917	agagactgtanacagtgaagcagatgctcttgaagcttcttcttactctccggagaaac		1976
Qy	1340	caaacccgaatgtgtacaaa-----	-----	1359

Dh	1977	caaacccgaaatggtcacaaagtgagtgagtcggaagtcggagaccctgtgttcaatcccttg	2035
Qy	1360	-----	1355
Dh	2037	ccccctgcctcaagggtgcacaaacctgatagtgtgcgcccaagccacagctctctcccaag	2096
Qy	1360	gtgaaattccctgcctctgtgaaagaaagaaagaaaccccttggcgcgtctgaagaccagcctgtgttgaaagag	1419
Dh	2097	gtgaactctgcctgcctctgtgaaagaaagaaagaaaccccttggcgcgtctgaagaccagcctgtgttgaaagag	2156
Qy	1420	ggagcgtcgtcggtgtgaaaccggccaatgggcatctctcaaccatcaacatcaacagccacaacatcaac	1479
Dh	2157	ggagcgtcgtcggtgtgaaaccggccaatgggcatctctcaaccatcaacatcaacagccacaacatcaac	2216
Qy	1480	gggaaagccgtctctcccgaaaccatctgtgtgcgtcggtgggcccaagcgggtgtatgtcttcag	1538
Dh	2217	gggaaagccgtctctcccgaaaccatctgtgtgcgtcggtgggcccaagcgggtgtatgtcttcag	2276
Qy	1540	a-----	1540
Dh	2277	aagtggtgtgtgagagagacaggggtgcgccctctcttgaacgggcacccggctgggggtctc	2336
Qy	1541	-----	1559
Dh	2337	tggcaagggtctgggggtgtgtgacaaagcacctgtctctcccaagcgtctaaatagaatttt	2396
Qy	1560	caactcccgccgagagacagccggaaagcaactctctgtgacaagtgtctgaaagaaataagaaatcccggt	1619
Dh	2397	caactcccgccgagagacagccggaaagcaactctctgtgacaagtgtctgaaagaaataagaaatcccggt	2456
Qy	1620	taataccaacctgtgtcaatgtga-----	1642
Dh	2457	taattaccacacctgtgtcaatgtgaagtgaggtcagagcccaaggttcccaagagtaaccag	2516
Qy	1643	-----	1642
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Qy	1643	--	1699
Dh	2577	ctcaaggtgagaaacaatcacatccaatgtgccctctgaactgtgacgcgaaatgtgtcaacttgggtga	2636
Qy	1700	ttcttccctgggcggagaaatcatccaagcccaacggtaaatgtatccctgcagatcatgtctct	1759
Dh	2637	ttcttccctgggcggagaaatcatccaagcccaacggtaaatgtatccctgcagatcatgtctct	2696
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Dh	2697	ggaaaggttaaaagagagccgggtgcaagcttgcgcccccaactctgaaaaacggtgggacatctg	2756
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Dh	2817	ctgtgtgtgtgtgagcgtgtgggaaagcgtgtatgaagaaagaaatccccgtctccggacaacatctc	2876
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AC	19-DEC-2000 (first entry)		
DT	Mouse methylentetrahydrofolate reductase gene.		
XX	Methylenetetrahydrofolate reductase; MTHFR; mouse; gene therapy;		
KW	diagnosis; Chromosome 4; ds.		
XX	Mus musculus.		
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XX	Mus musculus.		
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PR	01-MAR-1999; 99US-0258928.

PA (UYMC-) UNIV MCGILL.

PI Rozen R, Goyette P;

DR WPI; 2000-572192/53.

PT cDNA probe for the h

PT which is associated

PS Disclosure; Fig 13A-

CC The present sequence

CC the NADPH-linked red

CC homocysteine to meth

CC human MTHFR gene (see

CC models for MTHFR def

CC disorders.

SQ Sequence 3181 BP; 71

Best Local Similarity

1

[illegible]

2

A

100

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114	cagcagtgagtgagagcgtccaaagaatagtttcgagatgttccacccgcgagctgagacc	173		
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QY 246 -----aaggtttgaccggatgagcag 268
Db 354 tttaaccagagagcctaacttaaggagaatccctacaggttttgcacggatgagcagag 413
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DT 03-JAN-2002 (first entry)

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KW antisense therapy; EC 1.5.1.20; chromosome 1p36.3; cancer; kidney cell;
KW pancreas; lung; brain; cytostatic; colon carcinoma; breast; colorectal;
KW neuroblastoma; leukaemia; ds.
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OS Homo sapiens.
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XX US2001025030-A1.
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XX 01-MAR-1999; 99US-0258928.
XX
XX (ROZEN/ ROZEN R.
XX (SEKH/) SEKHON J.
XX
XX Rozen R, Sekhon J;
XX
XX WPI: 2001-638509/73.
XX
XX New antisense nucleic acids, which are methylenetetrahydrofolate
XX reductase inhibitors, useful for treating, stabilizing or preventing
XX cancer, e.g. breast carcinoma, colon carcinoma, colorectal carcinoma or
XX neuroblastoma
XX
XX Disclosure: Fig 12B; 68pp; English.
XX
XX The invention relates to a non allele-specific antisense nucleic acids,
XX which binds to methylenetetrahydrofolate reductase (MTHFR; EC 1.5.1.20)
XX nucleic acids and inhibits MTHFR protein expression in a mammal. MTHFR
XX catalyses the NADPH-linked reduction of 5,10-methylenetetrahydrofolate to
XX 5-methylenetetrahydrofolate, a co-substrate for methylation of
XX homocysteine to methionine. The invention provides potential therapy for
XX individuals with MTHFR deficiency. The non allele-specific antisense
XX nucleic acids are useful for treating, stabilizing or preventing cancer,
XX particularly breast carcinoma, colon carcinoma, colorectal carcinoma,
XX lung cancer, brain cancer, pancreatic cancer, kidney cell cancer,
XX neuroblastoma, glioma and leukaemia. MTHFR cDNA probe is used in gene
XX therapy. The present DNA sequence is human methylenetetrahydrofolate
XX reductase (MTHFR) gene exon 11 with flanking intron sequences. Human
XX MTHFR gene is mapped to chromosome 1p36.3.
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XX cancer; gene therapy; ds.
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Db 8258 GGGAACTAGTACTCTCTGCTCA 8235

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ID AAC49168 standard; DNA; 1942 BP.
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DT 18-OCT-2000 (first entry)
XX
DE Arabidopsis thaliana DNA fragment SEQ ID NO: 60181.
XX
KM Hybridisation assay; genetic mapping; gene expression control;
KM protein identification; signal transduction pathway;
KM metabolic pathway; promoter; termination sequence; ss.
XX
OS Arabidopsis thaliana.
XX
PN EP1033405-A2.
XX
PD 06-SEP-2000.
XX
PF 25-FEB-2000; 2000EP-0301439.
XX
XX 25-FEB-1999; 99US-0121825.
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PR 09-MAR-1999; 99US-0123548.
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DB 73 ccaagagcagaagatgagtcgacaatctcttgagagatgatcgatgtgtgtctat 132
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AAD20479;

AC AAD20479;

XX 03-JAN-2002 (first entry)

DE Human MTHFR gene exon 5 with partial Intron sequence.

XX Human: methylentetrahydrofolate reductase; MTHFR; gene therapy; glioma;
 KW antisense therapy; EC 1.5.1.20; chromosome 1p36.3; cancer; kidney cell;
 KW pancreas; lung; brain; cytosolic; colon carcinoma; breast; colorectal;
 KW neuroblastoma; leukemia; ds.

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XX FH Key Location/Qualifiers
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FT FT /partial
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FT FT exon /*tag= b
FT FT /number= 5
FT FT Intron /*tag= c
FT FT 292..341
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XX PN US2001025030-A1.
XX PD 27-SEP-2001.
XX PF 01-DEC-2000; 2000US-0728910.
XX PR 01-MAR-1999; 99US-0258928.
XX PA (ROZE/) ROZEN R.
XX PA (SEKH/) SEKHON J.
XX PI Rozen R, Sekhon J;
XX DR WPI: 2001-638509/73.
XX XX
XX PT New antisense nucleic acids, which are methylentetrahydrofolate
XX PT reductase inhibitors, useful for treating, stabilizing or preventing
XX PT cancer, e.g. breast carcinoma, colon carcinoma, colorectal carcinoma or
XX PT neuroblastoma -
XX PS Disclosure: Fig 12A; 68pp; English.
XX XX
XX CC The invention relates to a non allele-specific antisense nucleic acid,
XX CC which binds to methylentetrahydrofolate reductase (MTHFR; EC 1.5.1.20)
XX CC nucleic acids and inhibits MTHFR protein expression in a mammal. MTHFR
XX CC catalyses the NADPH-linked reduction of 5,10-methylentetrahydrofolate to
XX CC 5-methylentetrahydrofolate, a co-substrate for methylation of
XX CC homocysteine to methionine. The invention provides potential therapy for
XX CC individuals with MTHFR deficiency. The non allele-specific antisense
XX CC nucleic acids are useful for treating, stabilizing or preventing cancer,
XX CC particularly breast carcinoma, colon carcinoma, colorectal carcinoma,
XX CC lung cancer, brain cancer, pancreatic cancer, kidney cell cancer,
XX CC neuroblastoma, glioma and leukemia. MTHFR cDNA probe is used in gen-
XX CC therapy. The present DNA sequence is human methylentetrahydrofolate
XX CC reductase (MTHFR) gene exon 5 with flanking intron sequences. Human M HFR
XX CC gene is mapped to chromosome 1p36.3.
XX SQ Sequence 341 BP; 74 A; 105 C; 106 G; 56 T; 0 other;

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Query Match 11.6%; Score 255.4; DB 22; Length 341;
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DB 218 ttctacacctcaaccgcgcgatgtctaccacagaggtctcgaagccctcctgggatatg 277
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RESULT 13
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XX Arabidopsis thaliana DNA fragment SEQ ID NO: 38803.
XX Hybridisation assay; genetic mapping; gene expression control;
KW protein identification; signal transduction pathway;
KW metabolic pathway; promoter; termination sequence; ss.
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XX 25-FEB-2000; 2000EP-0301439.
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Query Match 11.4%; Score 250.8; DB 21; Length 1821;
Best Local Similarity 53.4%; Pred No. 166-485;
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OY 691 acgcaactttctttagagctgacacattcttcgcttggaaagcgatgcacacatg 750
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DB 670 gggaattgtgtcccatgttccctgggaattatgctatttaactaactaagagcttttg 729
OY 811 cagcttctgaagctgtccaaagctggaggtgcacagagatcaagagctgattgagca 870
DB 730 cgtatgactgtttcttcgaagactaagatacagatgagtgagtgagctgcgttggagcct 789
OY 871 atcaagaacaaagatgctgcattccgaactatgcatgagctggcggtgagctgtgc 930
DB 790 atcaagatacagaagaagcgtggaagccatagttatccacttggaaacagagatglt 849
OY 931 caggagcttctggaagctgtgtgccaagctcccaatctcaaccccaacagcgag 990
DB 850 aaaaagatgttgcgtatcgatgagtcagttc---ctcatcctcatcattgaaacatgag 906
OY 991 atggtctcaacagaagtgctggaagcgctggagatgtgactgagaccca---ggcgt 1047
DB 907 aaatctgctcttgaatattgatatcttggatgattgagttcacaatttctcgt 966
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DB 967 tcttaaccctggagagcgcccttgcacaatgtttccgtatcaggaagatgtgcgcccat 1026
OY 1108 ttctgggctctcagacaaagattacatcagtaaccagagatgtagacgtttccct 1167
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OY 1288 ancaigtgaagcaagtgtcttngaagttcttcttaactctcggagagaacaaacgg 1347
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Oy      1828 ccacacatcatccagtaacacccagcaactctctctgtcaactgtgtgacatgac 1887
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Oy      1888 ttc 1890
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RESULT 14
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AC      AAd20475;
XX      03-JAN-2002 (first entry)
XX      Human MTHFR gene exon 1 with partial intron sequence.
XX      Human; methylenetetrahydrofolate reductase; MTHFR; gene therapy; glioma;
KW      antisense therapy; EC 1.5.1.20; chromosome 1p36.3; cancer; kidney cell;
KW      pancreas; lung; brain; cytostatic; colon carcinoma; breast; colorectal;
XX      neuroblastoma; leukaemia; ds.
XX      Homo sapiens.
OS      Homo sapiens.
FH      Key
FH      intron
FT      1.50
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FT      /partial
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FT      /tag- c
FT      /number- 2
FT      /partial
FT      intron
PN      US2001025030-A1.
XX      27-SEP-2001.
XX      01-DEC-2000; 2000US-0728910.
XX      01-MAR-1999; 99US-0258928.
XX      (ROZEN/) ROZEN R.
XX      (SEKH/) SEKHON J.
XX      Rozen R, Sekhon J;
XX      WPI; 2001-638509/73.
XX      DR
XX      PT New antisense nucleic acids, which are methylenetetrahydrofolate
XX      PT reductase inhibitors, useful for treating, stabilizing or preventing
XX      PT cancer, e.g. breast carcinoma, colon carcinoma, colorectal carcinoma or
XX      PT neuroblastoma
XX      PS
XX      PS Disclosure; Fig 12A; 68pp; English.
XX      CC The invention relates to a non allele-specific antisense nucleic acids,
XX      CC which binds to methylenetetrahydrofolate reductase (MTHFR; EC 1.5.1.20)
XX      CC nucleic acids and inhibits MTHFR protein expression in a mammal. MTHFR
XX      CC catalyses the NADPH-linked reduction of 5,10-methylenetetrahydrofolate to
XX      CC 5-methylenetetrahydrofolate, a co-substrate for methylation of
XX      CC homocysteine to methionine. The invention provides potential therapy for
XX      CC individuals with MTHFR deficiency. The non allele-specific antisense
XX      CC nucleic acids are useful for treating, stabilizing or preventing cancer,
XX      CC particularly breast carcinoma, colon carcinoma, colorectal carcinoma,

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CC      Lung cancer, brain cancer, pancreatic cancer, kidney cell cancer,
CC      neuroblastoma, glioma and leukaemia. MTHFR cDNA probe is used in gene
CC      therapy. The present DNA sequence is human methylenetetrahydrofolate
CC      reductase (MTHFR) gene exon 1 with flanking intron sequences. Human MTHFR
CC      gene is mapped to chromosome 1p36.3.
XX      SQ
XX      Sequence 346 BP; 75 A; 92 C; 113 G; 66 T; 0 other;

Query Match      11.0%; Score 242; DB 22; Length 346;
Best Local Similarity 100.0%; Pred. No. 1.le-46;
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Oy      189 gtctccctggaaatctctccctccctcgaaactgctgagggagcgtgcaatcattcaag 248
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XX      Human MTHFR gene exon 2 with partial intron sequence.
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KW      antisense therapy; EC 1.5.1.20; chromosome 1p36.3; cancer; kidney cell;
KW      pancreas; lung; brain; cytostatic; colon carcinoma; breast; colorectal;
XX      neuroblastoma; leukaemia; ds.
XX      OS
XX      OS Homo sapiens.
XX      FH
XX      FH Key
XX      FH intron
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XX      27-SEP-2001.
XX      01-DEC-2000; 2000US-0728910.
XX      01-MAR-1999; 99US-0258928.
XX      (ROZEN/) ROZEN R.

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PA (SEKH/) SEKHON J.

XX Rozen R, Sekhon J;

XX WPI; 2001-638509/73.

DR
XX
XX
PT New antisense nucleic acids, which are methylenetetrahydrofolate
PT reductase inhibitors, useful for treating, stabilizing or preventing
PT cancer, e.g. breast carcinoma, colon carcinoma, colorectal carcinoma or
PT neuroblastoma

PS Disclosure; Fig 12A: 68pp; English.

XX
XX
CC The invention relates to a non allele-specific antisense nucleic acids,
CC which binds to methylenetetrahydrofolate reductase (MTHFR; EC 1.5.1.20)
CC nucleic acids and inhibits MTHFR protein expression in a mammal. MTHFR
CC catalyses the NADPH-linked reduction of 5,10-methylenetetrahydrofolate to
CC 5-methylenetetrahydrofolate, a co-substrate for methylation of
CC homocysteine to methionine. The invention provides potential therapy for
CC individuals with MTHFR deficiency. The non allele-specific antisense
CC nucleic acids are useful for treating, stabilizing or preventing cancer,
CC particularly breast carcinoma, colon carcinoma, colorectal carcinoma,
CC lung cancer, brain cancer, pancreatic cancer, kidney cell cancer,
CC neuroblastoma, glioma and leukaemia. MTHFR cDNA probe is used in gene
CC therapy. The present DNA sequence is human methylenetetrahydrofolate
CC reductase (MTHFR) gene exon 2 with flanking intron sequences. Human MTHFR
CC gene is mapped to chromosome 1p36.3.

XX
SO Sequence 339 BP; 73 A; 108 C; 95 G; 63 T; 0 other;

Query Match 10.9%; Score 240.2; DB 22; Length 339;
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Matches 242; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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QY 303 agcaggtgacctggctcacaagaagagacctctccatgatatgcccagcaccgcgt 362
DB |||||
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QY 363 gaactactgtgacctgagagacacatctgacatgacctgtgcgtcagcgcctggagga 422
DB |||||
DB 165 gaactactgtgacctgagagacacatctgacatgacctgtgcgtcagcgcctggagga 224
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GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: June 26, 2002, 15:32:23 ; Search time 82.36 Seconds
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Title: SEQ1MOD

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Searched: 383533 seqs, 122816752 residues

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	2186.6	99.6	2220	4	US-09-258-928-1
5	2177.6	99.2	2187	4	US-09-318-448-1
6	119	5.4	120	4	US-09-218-114A-5
7	67.2	3.1	4848	4	US-08-955-957A-1
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9	67.2	3.1	4848	4	US-08-955-957A-6
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17	40.4	1.8	2155	2	US-08-095-728B-5
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24	38.4	1.7	4858	3	US-08-436-332B-9
25	37.6	1.7	7218	1	US-08-232-463-14
26	37.6	1.7	7808	2	US-08-149-097D-22
27	37.2	1.7	7791	2	US-08-149-097D-23

28	37	1.7	510	4	US-09-516-914-8	Sequence 8, Appl1
29	37	1.7	14272	4	US-09-516-914-23	Sequence 23, Appl1
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31	36.8	1.7	2481	1	US-08-324-243-35	Sequence 35, Appl1
32	36.8	1.7	2481	1	US-08-532-390-35	Sequence 35, Appl1
33	36.8	1.7	2481	3	US-08-717-294-35	Sequence 35, Appl1
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35	36.8	1.7	3545	3	US-08-480-474-10	Sequence 10, Appl1
36	36.8	1.7	4808	2	US-08-231-193A-10	Sequence 10, Appl1
37	36.8	1.7	4808	2	US-08-486-273A-10	Sequence 10, Appl1
38	36.8	1.7	4808	3	US-08-940-086A-10	Sequence 10, Appl1
39	36.8	1.7	4808	4	US-08-940-035A-10	Sequence 10, Appl1
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41	36.4	1.7	309	4	US-09-221-298-4	Sequence 44, Appl1
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44	36.2	1.6	624	4	US-09-281-221-3	Sequence 3, Appl1
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ALIGNMENTS

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; Patent No. 6074821
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; NUMBER OF INVENTION: REDUCTASE
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: KLAUBER & JACKSON
; STREET: Continental Plaza - 411 Hackensack Avenue
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: U.S.A.
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/738,000
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/CA95/00314
; FILING DATE: 25-MAY-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9410620.0
; FILING DATE: 26-MAY-1994
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2219 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 13..1983
; US-08-738-000-3

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Best Local Similarity 99.7%; Pred. No. 0;
Matches 2189; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
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GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: June 26, 2002, 15:41:08 ; Search time 3727.78 Seconds
(without alignments)
12744.915 Million cell updates/sec

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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 21979536 seqs, 10817449327 residues

Total number of hits satisfying chosen parameters: 43959072

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database :

Pending_Patents_NA_Main:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	2188	99.6	2196	36	US-09-962-667-15
4	2188	99.6	2196	36	US-09-963-333-15
5	2186.6	99.6	2196	31	US-09-802-640-33
6	2186.6	99.6	2219	22	US-09-592-595-3
7	2186.6	99.6	2219	26	US-09-660-872-3
8	2186.6	99.6	2219	26	US-09-660-872-3
9	2186.6	99.6	2219	26	US-09-660-872-3
10	2186.6	99.6	2219	26	US-09-660-872-3
11	2186.6	99.6	2220	22	US-09-728-910-3
12	2186.6	99.6	2220	22	US-09-592-595A-1
13	2186.6	99.6	2220	26	US-09-660-872-1
14	2186.6	99.6	2220	26	US-09-660-872-1
15	2186.6	99.6	2220	26	US-09-660-872-1
16	2177.6	99.2	2187	17	US-09-371-347-51
17	2173.8	99.0	3485	66	US-60-278-258-99
18	2173.8	99.0	5979	71	US-60-324-185-1968
19	2172.2	98.9	2340	18	US-09-471-275-2157
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33 433.2 19.7 18542 1 PCT-US01-26488-1 Sequence 1, Appl
34 333.4 17.9 489 16 US-09-277-227-19340 Sequence 19340, A
35 333.4 17.9 489 17 US-09-346-956-16939 Sequence 16939, A
36 333.4 17.9 489 34 US-09-904-703-16939 Sequence 16939, A
37 333.4 17.9 489 34 US-09-909-627-19340 Sequence 19340, A
38 333.2 17.9 399 17 US-09-362-510-58537 Sequence 58537, A
39 333.2 17.9 399 17 US-09-362-510-58537 Sequence 58537, A
40 333.2 17.9 399 34 US-09-904-013-58537 Sequence 58537, A
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43 373.8 17.0 378 19 US-09-528-409-52118 Sequence 52118, A
44 373.8 17.0 378 35 US-09-933-524-52118 Sequence 52118, A
45 373.8 17.0 378 35 US-09-933-524A-52118 Sequence 52118, A
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ALIGNMENTS

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; Sequence 15 Application US/09658659
; GENERAL INFORMATION:
; APPLICANT: Stanton, Jr., Vincent P.
; TITLE OF INVENTION: GENE SEQUENCE VARIANCE IN GENES RELATED
; TITLE OF INVENTION: TO FOLATE METABOLISM HAVING UTILITY IN DETERMINING THE
; FILE REFERENCE: 11926-015001
; CURRENT APPLICATION NUMBER: US/09/658,659
; PRIOR FILING DATE: 2000-09-08
; PRIOR APPLICATION NUMBER: 09/596,033
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 09/357,743
; PRIOR FILING DATE: 1999-07-20
; PRIOR APPLICATION NUMBER: 09/357,024
; PRIOR FILING DATE: 1999-07-19
; PRIOR APPLICATION NUMBER: 60/093,484
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15
; LENGTH: 2196
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; ORGANISM: Artificial Sequence
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; LOCATION: 1784
; OTHER INFORMATION: n = a or g
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US-09-658-659-15
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RESULT 2
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 : Sequence 15, Application US/09962665
 : GENERAL INFORMATION:
 : APPLICANT: Stanton, Jr., Vincent P.

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: TITLE OF INVENTION: POLY(POLYGLUTAMATE SYNTHETASE GENE SEQUENCE
: TITLE OF INVENTION: VARIANCES HAVING UTILITY IN DETERMINING THE
: FILE REFERENCE: 11926-015004
: CURRENT APPLICATION NUMBER: US/09/962,665
: PRIOR FILING DATE: 2001-09-24
: PRIOR APPLICATION NUMBER: 09/658,659
: PRIOR FILING DATE: 2000-09-08
: PRIOR APPLICATION NUMBER: 09/596,033
: PRIOR FILING DATE: 2000-06-15
: PRIOR APPLICATION NUMBER: 09/357,743
: PRIOR FILING DATE: 1999-07-20
: PRIOR APPLICATION NUMBER: 09/357,024
: PRIOR FILING DATE: 1999-07-19
: PRIOR APPLICATION NUMBER: 60/093,484
: PRIOR FILING DATE: 1998-07-20
: NUMBER OF SEQ. ID NOS: 16
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ. ID NO. 15
: LENGTH: 2196
: TYPE: DNA
: ORGANISM: Artificial Sequence
: FEATURE:
: OTHER INFORMATION: Synthetic construct
: NAME/KEY: misc-feature
: LOCATION: 1784
: OTHER INFORMATION: n = a or g
: NAME/KEY: misc-feature
: LOCATION: 464
: OTHER INFORMATION: n = g or t
: NAME/KEY: misc-feature
: LOCATION: 120, 519, 668, 1059, 1308
: OTHER INFORMATION: n = c or t
: NAME/KEY: misc-feature
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: US-09-962-665-15

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Query Match 99.6%; Score 2188; DB 36; Length 2196;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 2191; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 aattccggagccatgtgtgagagagccagaggaagagcagctcaaccctgttgag 60
Db 1 aattccggagccatgtgtgagagagccagaggaagagcagctcaaccctgttgag 60

Qy 61 ggcagtgccagcagtgagcagtgagagctccaaagatgttcagatgttccaccgggc 120
Db 61 ggcagtgccagcagtgagcagtgagagctccaaagatgttcagatgttccaccgggc 120

Qy 121 ctggagccctgagcagcagtgagagagctccgaggaagatgagcgagatgtgaactgt 180
Db 121 ctggagccctgagcagcagtgagagagctccgaggaagatgagcgagatgtgaactgt 180

Qy 181 gacaagtgttctccctggaattcttccctcctggaactgctgagggagggctgaattc 240
Db 181 gacaagtgttctccctggaattcttccctcctggaactgctgagggagggctgaattc 240

Qy 241 altcaaggtttgacccgagtgagcagcaggttgagccctctacatagagcgtgagcagc 300
Db 241 altcaaggtttgacccgagtgagcagcaggttgagccctctacatagagcgtgagcagc 300

Qy 301 cgaagaggttgacccctggtgttcagacaagagagactctccatgatatgctcagcagcc 360
Db 301 cgaagaggttgacccctggtgttcagacaagagagactctccatgatatgctcagcagcc 360

Qy 361 gtaactactgtgcttgagagaccatctctgacatgactgtgctgctcagcgctggag 420
Db 361 gtaactactgtgcttgagagaccatctctgacatgactgtgctgctcagcgctggag 420

Qy 421 gagatcacgggacatctgacacaagctaaagcagctggcgctgaggaacatctggcgctg 480

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Db 421 gaatacagggccatctgcaacaagcagctggcctgangaacatcatgycgtg 480
QY 481 cggggaaccacaaatagtgaccagtggaagaggaagaggttcaactacagcagt 540
Db 481 cggggaaccacaaatagtgaccagtggaagaggaagaggttcaactacagcagt 540
QY 541 gacctgtgaagacacatccgaatgagttgtgactacttgaactcgtgtgcaagt 600
Db 541 gacctgtgaagacacatccgaatgagttgtgactacttgaactcgtgtgcaagt 600
QY 601 taacccaaagccaccgcaagcaggaagccttgagctgactgaagcactgaagag 660
Db 601 taacccaaagccaccgcaagcaggaagccttgagctgactgaagcactgaagag 660
QY 661 aaggtgtgagcaggaagcagcattcatcatcagcagccttcttgaagctgaacac 720
Db 661 aaggtgtgagcaggaagcagcattcatcatcagcagccttcttgaagctgaacac 720
QY 721 ttcgccttgtgaagcagcagcagcagcagcagcagcagcagcagcagcagcagc 780
Db 721 ttcgccttgtgaagcagcagcagcagcagcagcagcagcagcagcagcagcagc 780
QY 781 ttccaccacagagcagcagcagcagcagcagcagcagcagcagcagcagcagc 840
Db 781 ttccaccacagagcagcagcagcagcagcagcagcagcagcagcagcagcagc 840
QY 841 ccaacagagatcaagagcagcagcagcagcagcagcagcagcagcagcagcagc 900
Db 841 ccaacagagatcaagagcagcagcagcagcagcagcagcagcagcagcagcagc 900
QY 901 tatgcatcagacgtgagcagcagcagcagcagcagcagcagcagcagcagcagc 960
Db 901 tatgcatcagacgtgagcagcagcagcagcagcagcagcagcagcagcagcagc 960
QY 961 ggcctcacttcaacacccctcaacccgagagtgctacacacagagtgctgaagcgc 1020
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QY 1141 cgtaccagagtgagcagcagcagcagcagcagcagcagcagcagcagcagcagc 1200
Db 1141 cgtaccagagtgagcagcagcagcagcagcagcagcagcagcagcagcagcagc 1200
QY 1201 ttgggagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 1260
Db 1201 ttgggagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 1260
QY 1261 ctgctgaagatgtgagcagcagcagcagcagcagcagcagcagcagcagcagc 1320
Db 1261 ctgctgaagatgtgagcagcagcagcagcagcagcagcagcagcagcagcagc 1320
QY 1321 ctttaacctctgggagacacaaacccggaatggtcaacaaagtacttgcctctgag 1380
Db 1321 ctttaacctctgggagacacaaacccggaatggtcaacaaagtacttgcctctgag 1380
QY 1381 gatgagccctggcagcagcagcagcagcagcagcagcagcagcagcagcagcag 1440
Db 1381 gatgagccctggcagcagcagcagcagcagcagcagcagcagcagcagcagcag 1440
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Db 1441 caggagcctcctacacatcaactcaacagcccaacatcaacaggaagcgtctccgaccc 1500
QY 1501 atcgtgagcctggcagcagcagcagcagcagcagcagcagcagcagcagcagcag 1560
Db 1501 atcgtgagcctggcagcagcagcagcagcagcagcagcagcagcagcagcagcag 1560
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Db 1561 actcccgagagcagcaggaagcagcagcagcagcagcagcagcagcagcagcagc 1620
QY 1621 aattaccacctgtcaatgtgaaggggtgaataaatacaacaaatgcccctgaatgcagcc 1680
Db 1621 aattaccacctgtcaatgtgaaggggtgaataaatacaacaaatgcccctgaatgcagcc 1680
QY 1681 aatgctgtaacttgaggagcagcagcagcagcagcagcagcagcagcagcagcagc 1740
Db 1681 aatgctgtaacttgaggagcagcagcagcagcagcagcagcagcagcagcagcagc 1740
QY 1741 cccgtcagcttcatgtctgtgaagagcagcagcagcagcagcagcagcagcagcagc 1800
Db 1741 cccgtcagcttcatgtctgtgaagagcagcagcagcagcagcagcagcagcagcagc 1800
QY 1801 aagctgtatgagagagagcagcagcagcagcagcagcagcagcagcagcagcagc 1860
Db 1801 aagctgtatgagagagagcagcagcagcagcagcagcagcagcagcagcagcagc 1860
QY 1861 ttctgttcaacctgtgtgaacatagcagcagcagcagcagcagcagcagcagcagcagc 1920
Db 1861 ttctgttcaacctgtgtgaacatagcagcagcagcagcagcagcagcagcagcagcagc 1920
QY 1921 gaagacacatgtgagcagcagcagcagcagcagcagcagcagcagcagcagcagc 1980
Db 1921 gaagacacatgtgagcagcagcagcagcagcagcagcagcagcagcagcagcagc 1980
QY 1981 tgacctgtctcctgaagcagcagcagcagcagcagcagcagcagcagcagcagcagc 2040
Db 1981 tgacctgtctcctgaagcagcagcagcagcagcagcagcagcagcagcagcagcagc 2040
QY 2041 gtgctgtctctctgtggaactcagcagcagcagcagcagcagcagcagcagcagcagc 2100
Db 2041 gtgctgtctctctgtggaactcagcagcagcagcagcagcagcagcagcagcagcagc 2100
QY 2101 cccacccagacatgagcagcagcagcagcagcagcagcagcagcagcagcagcagc 2160
Db 2101 cccacccagacatgagcagcagcagcagcagcagcagcagcagcagcagcagcagc 2160
QY 2161 tcggcccaatgaggaactagtaactctctgctcta 2196
Db 2161 tcggcccaatgaggaactagtaactctctgctcta 2196

RESULT 3
US-09-962-677-15
; Sequence 15, Application US/09962677
; GENERAL INFORMATION:
; APPLICANT: Stanton, Jr., Vincent P.
; TITLE OF INVENTION: THYMIDINE PHOSPHORYLASE GENE SEQUENCE
; TITLE OF INVENTION: VARIANCES HAVING UTILITY IN DETERMINING
; FILE REFERENCE: 11926-015003
; CURRENT FILING DATE: 2001-09-24
; PRIOR APPLICATION NUMBER: 09/658,659
; PRIOR FILING DATE: 2000-09-08
; PRIOR APPLICATION NUMBER: 09/596,033
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 09/357,743
; PRIOR FILING DATE: 1999-07-20
; PRIOR APPLICATION NUMBER: 09/357,024
; PRIOR FILING DATE: 1999-07-19
; PRIOR APPLICATION NUMBER: 60/093,484
; PRIOR FILING DATE: 1998-07-20
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15
; LENGTH: 2196
; TYPE: DNA
; ORGANISM: Artificial Sequence
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Db 1861 ttccctgtcaacctgtgtgaacatgacttcccaactggaacactgctctgtgagtggtg 1920
Qy 1921 gaagacacatttgagcttctcaacagcccccacaaatgagagaaacagaggtctca 1980
Db 1921 gaagacacatttgagcttctcaacagcccccacaaatgagagaaacagaggtctca 1980
Qy 1981 tgacctgtctctgtgagacctgctgtgagacctctctccgacctctctccaca 2040
Db 1981 tgacctgtctctgtgagacctgctgtgagacctctctccgacctctctccaca 2040
Qy 2041 gtgtgtctctctgtgagacctgctgtgagacctctctccgacctctctccaca 2100
Db 2041 gtgtgtctctctgtgagacctgctgtgagacctctctccgacctctctccaca 2100
Qy 2101 ccccaactgacaatgagcaactgagctgagtgaggttccagactcttcttgagactgag 2160
Db 2101 ccccaactgacaatgagcaactgagctgagtgaggttccagactcttcttgagactgag 2160
Qy 2161 tcggcccaatgagcaactgagctgagtgaggttccagactcttcttgagactgag 2160
Db 2161 tcggcccaatgagcaactgagctgagtgaggttccagactcttcttgagactgag 2160

RESULT 4
US-09-963-333-15
; Sequence 15, Application US/09963333
; GENERAL INFORMATION:
; APPLICANT: Stanton, Jr., Vincent P.
; TITLE OF INVENTION: THYMIDINE SYNTHASE GENE SEQUENCE VARIANCES
; TITLE OF INVENTION: HAVING UTILITY IN DETERMINING THE TREATMENT
; FILE REFERENCE: 11926-015002
; CURRENT FILING DATE: 2001-09-24
; PRIOR APPLICATION NUMBER: US/09/963,333
; PRIOR FILING DATE: 2000-09-08
; PRIOR APPLICATION NUMBER: 09/596,033
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 09/357,743
; PRIOR FILING DATE: 1999-07-20
; PRIOR APPLICATION NUMBER: 09/357,024
; PRIOR FILING DATE: 1999-07-19
; PRIOR APPLICATION NUMBER: 60/093,484
; PRIOR FILING DATE: 1998-07-20
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15
; LENGTH: 2196
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic construct
; NAME/KEY: misc_feature
; LOCATION: 1784
; OTHER INFORMATION: n = a or g
; NAME/KEY: misc_feature
; LOCATION: 464
; OTHER INFORMATION: n = g or t
; NAME/KEY: misc_feature
; LOCATION: 120, 519, 668, 1059, 1308
; OTHER INFORMATION: n = c or t
; NAME/KEY: misc_feature
; LOCATION: 1289
; OTHER INFORMATION: n = c or a
; OTHER INFORMATION: n = c or a
US-09-963-333-15

Query Match 99.6%; Score 2188; DB 36; Length 2196;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 2191; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
Qy 1 aatccgagccatgtgtgaacgaagccagaggaacagcagctcaacccctgttgag 60

Db 1 aatccgagccatgtgtgaacgaagccagaggaacagcagctcaacccctgttgag 60
Qy 61 ggcagtgccagcagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgag 120
Db 61 ggcagtgccagcagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgag 120
Qy 121 ctggaacctgaagcagcagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgag 180
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Qy 181 gacaagtgtgtctctctgtgaattctctctctctctctctctctctctctctctctctc 240
Db 181 gacaagtgtgtctctctgtgaattctctctctctctctctctctctctctctctctctc 240
Qy 241 atctcaaggtttacccgagtgagcagcagtgagcagcagtgagcagcagtgagcagcag 300
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Db 301 ccaagcagtgagcagtgagcagcagtgagcagcagtgagcagcagtgagcagcagtgag 360
Qy 361 gtaactactgt 420
Db 361 gtaactactgt 420
Qy 421 gagatcagcagcagtgagcagcagtgagcagcagtgagcagcagtgagcagcagtgag 480
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Qy 481 cgggagagcccaatgaagtgagcagtgaggaaggaaggaaggaaggaaggaaggaagga 540
Db 481 cgggagagcccaatgaagtgagcagtgaggaaggaaggaaggaaggaaggaaggaagga 540
Qy 541 gacctgtgagagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcag 600
Db 541 gacctgtgagagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcag 600
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Db 601 taaccacaagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcag 660
Qy 661 aaggt 720
Db 661 aaggt 720
Qy 721 ttccgcttgtagagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcag 780
Db 721 ttccgcttgtagagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcag 780
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Db 781 ttcccaatcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcag 840
Qy 841 ccaagagagatcagagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 900
Db 841 ccaagagagatcagagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 900
Qy 901 tatgcatcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 960
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Db 1081 cgcagagagagagatgagcagcagcagcagcagcagcagcagcagcagcagcagcagcag 1140

Db 1081 cgcgagagagatgatacctccatcttcctggtcccaagacaaagtatacatctac 1140
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QY 1381 gatgaagcccttggcggtgaaagacagcctgtgaaagagagagctgtgctgaacgcg 1440
Db 1381 gatgaagcccttggcggtgaaagacagcctgtgaaagagagagctgtgctgaacgcg 1440
QY 1441 caggagcctccacacatcaactcaagcccaacatcaaggggaagcgtcctccgaccc 1500
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QY 1501 atcgtggtgctggggcccaagcggtgctatgtcttccgaagagcctcttgaagtcttc 1560
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QY 1561 attcccgcgagagacgggaagcaactctctgaagtgctgaaagagtaagagctcgggt 1620
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Db 1621 aattaccacctgtgcaatgtgaaaggtgtaaaacatccacatgcccctgaagcagcg 1680
QY 1681 aatgctctcaatctggggacatcttccctggcgagagatactccagcccaagctagtgat 1740
Db 1681 aatgctctcaatctggggacatcttccctggcgagagatactccagcccaagctagtgat 1740
QY 1741 cccgtcagctcattgtcttgaaagacgagagccttggccctgtagattgagcggtggga 1800
Db 1741 cccgtcagctcattgtcttgaaagacgagagccttggccctgtagattgagcggtggga 1800
QY 1801 aagctgtatgagagagagagtcctccgtcccgacacatcatccagtaactccagcaactac 1860
Db 1801 aagctgtatgagagagagagtcctccgtcccgacacatcatccagtaactccagcaactac 1860
QY 1861 ttccgtgtaacctgtggaacatgacttcccaacttgaaacactgctctggcaggtgggtg 1920
Db 1861 ttccgtgtaacctgtggaacatgacttcccaacttgaaacactgctctggcaggtgggtg 1920
QY 1921 gaagacacattggaagcttctcaacagcccaacagaaatgagaaacgagaggtcca 1980
Db 1921 gaagacacattggaagcttctcaacagcccaacagaaatgagaaacgagaggtcca 1980
QY 1981 tgacctgtgctctgaagcctgtggttgagacacactgttcccgctccctcccaaca 2040
Db 1981 tgacctgtgctctgaagcctgtggttgagacacactgttcccgctccctcccaaca 2040
QY 2041 ggtgctgctctcttggaactcaactcctctcgtgtctctcccaacccggcctccactc 2100
Db 2041 ggtgctgctctcttggaactcaactcctctcgtgtctctcccaacccggcctccactc 2100
QY 2101 ccccaactgaaatgagcagctagactgaggtgaggtccacaggtcctccctggacgtgag 2160
Db 2101 ccccaactgaaatgagcagctagactgaggtgaggtccacaggtcctccctggacgtgag 2160
QY 2161 tcggcccaaatggaaactgactctctctcta 2196
Db 2161 tcggcccaaatggaaactgactctctctcta 2196

RESULT 5
US-09-802-640-33
Sequence 33, Application US/09802640
GENERAL INFORMATION:
APPLICANT: Braun, Andreas
APPLICANT: Bonsal Aruna
APPLICANT: Kiehn Patrick
TITLE OF INVENTION: GENES AND POLYMORPHISMS ASSOCIATED WITH
FILE REFERENCE: 24736-2048
CURRENT APPLICATION NUMBER: US/09/802,640
NUMBER OF SEQ ID NOS: 122
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 33
LENGTH: 2196
TYPE: DNA
ORGANISM: Homo sapien
FEATURE:
NAME/KEY: CDS
LOCATION: (13)...(1983)
OTHER INFORMATION: Nucleotide sequence encoding
US-09-802-640-33
5'-10-methylmetetrahydrofolate reductase (MTHFR)

Query Match 99.6%; Score 2186.6; DB 31; Length 2196;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 2189; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 aattccgagacatggtgaaagacgaagcgaaggaagcaagcagcctcaacccctgtggag 60
Db 1 aattccgagacatggtgaaagacgaagcgaaggaagcaagcagcctcaacccctgtggag 60
QY 61 ggcagtgccagcaggtgagctgagagatcccaagatagtcgaagtgtccaccccgagc 120
Db 61 ggcagtgccagcaggtgagctgagagatcccaagatagtcgaagtgtccaccccgagc 120
QY 121 ctggacccctgagcagctagagacatcccgagaaatgagagcgagcttgaaatcgt 180
Db 121 ctggacccctgagcagctagagacatcccgagaaatgagagcgagcttgaaatcgt 180
QY 181 gaaagtgttctccctggaatcttccctcctgaactgctgagagagctgtcaatc 240
Db 181 gaaagtgttctccctggaatcttccctcctgaactgctgagagagctgtcaatc 240
QY 241 attcaaggttgaacggatgagcagaggtggccctctacatgaaagtgaactgagac 300
Db 241 attcaaggttgaacggatgagcagaggtggccctctacatgaaagtgaactgagac 300
QY 301 ccaagcaggtgacccctggtcacaagaagagacatccctccatgatgatcgacagcgc 360
Db 301 ccaagcaggtgacccctggtcacaagaagagacatccctccatgatgatcgacagcgc 360
QY 361 gtaactactgtgagcctggaagacatctctgacatgaactgtcgcgtcaagcgctgag 420
Db 361 gtaactactgtgagcctggaagacatctctgacatgaactgtcgcgtcaagcgctgag 420
QY 421 gagatcaaggcgacatctgacaagaactaagcagcgtgggctgaaagaacatcagcgctg 480
Db 421 gagatcaaggcgacatctgacaagaactaagcagcgtgggctgaaagaacatcagcgctg 480
QY 481 cggggaagcccaatagtgaccagtgggaagagagagaggttcacaaactaagcgagtg 540
Db 481 cggggaagcccaatagtgaccagtgggaagagagagaggttcacaaactaagcgagtg 540
QY 541 gacctggtgaaagacatccgaaggtgaggttgtaactattgacatctgtgtgagag 600
Db 541 gacctggtgaaagacatccgaaggtgaggttgtaactattgacatctgtgtgagag 600
QY 601 taacccaaggccaccccgaaagcagaggtttagagctgacctgaagcactgaaagag 660

Db	601	laccacaagagccaccocgaagcagagagctttgaggtctgaactgaaacattgaaagag	660
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Db	661	aaggtctcgggagccgattcatcaatcaacgagctttcttggagctgacaattc	720
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US-09-592-595-3			
; Sequence 3, Application US/09592595			
GENERAL INFORMATION:			
APPLICANT: ROZEN, Rima			
TITLE OF INVENTION: CDNA FOR HUMAN METHYLENETETRAHYDROLATE			
TITLE OF INVENTION: REDUCTASE AND USES THEREOF			
FILE REFERENCE: 04844/005005			
CURRENT APPLICATION NUMBER: US/09/592,595			
CURRENT FILING DATE: 2000-06-12			
PRIOR APPLICATION NUMBER: US 09/258,928			
PRIOR FILING DATE: 1999-03-01			
PRIOR APPLICATION NUMBER: US 08/738,000			
PRIOR FILING DATE: 1997-02-12			
PRIOR APPLICATION NUMBER: PCT/CA95/00314			
PRIOR FILING DATE: 1995-05-25			
PRIOR APPLICATION NUMBER: GB 9410620.0			
PRIOR FILING DATE: 1994-05-26			
NUMBER OF SEQ ID NOS: 18			
SOFTWARE: FastSeq for Windows Version 4.0			
SEQ ID NO 3			
LENGTH: 2219			
TYPE: DNA			
ORGANISM: Homo sapiens			
FEATURE:			
NAME/KEY: CDS			
LOCATION: (13) ... (1983)			
US-09-592-595-3			

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RESULT 7

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; Sequence 3, Application US/09592595A
; GENERAL INFORMATION:
; APPLICANT: ROZEN, Rima
; TITLE OF INVENTION: CDNA FOR HUMAN METHYLENETETRAHYDROFOLATE
; FILE REFERENCE: 04844/005003
; CURRENT APPLICATION NUMBER: US/09/592,595A
; CURRENT FILING DATE: 2000-06-12
; PRIOR APPLICATION NUMBER: US 09/258,928
; PRIOR FILING DATE: 1999-03-01
; PRIOR APPLICATION NUMBER: US 08/738,000
; PRIOR FILING DATE: 1997-02-12
; PRIOR APPLICATION NUMBER: PCT/CA95/00314
; PRIOR FILING DATE: 1995-05-25
; PRIOR APPLICATION NUMBER: GB 9410620.0
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 2219
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (13)...(1983)
US-09-592-595A-3
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QY 1681 aatgtgtcactgtgggacatcttcctcgtgagagagatcaacacacacacacacacac 1740
```

Db 1681 aatgctgtaacttgggcaactcttccctgggcagagatcatccagcccaactagtgat 1740
QY 1741 ccgcgtacgttcatgtcttggaaagacagagccttggccctttagattgagcggtggga 1800
Db 1741 ccgcgtacgttcatgtcttggaaagacagagccttggccctttagattgagcggtggga 1800
QY 1801 aagctgtatgaaagagagtcctccgtccgcagccatcatccatcatccacagcaactac 1860
Db 1801 aagctgtatgaaagagagtcctccgtccgcagccatcatccatcatccacagcaactac 1860
QY 1861 ttccctgttcaactctgttgacaatacttccatctgcagacaatctgccttggcaggtgtg 1920
Db 1861 ttccctgttcaactctgttgacaatacttccatctgcagacaatctgccttggcaggtgtg 1920
QY 1921 gaagacacattggagcttcttcaacagcgccacccaagaaatgcaagaaacagagctcca 1980
Db 1921 gaagacacattggagcttcttcaacagcgccacccaagaaatgcaagaaacagagctcca 1980
QY 1981 tgacctgtcgtcttgacgacctgtgttgagacaaatctctgtccgccttccctccaca 2040
Db 1981 tgacctgtcgtcttgacgacctgtgttgagacaaatctctgtccgccttccctccaca 2040
QY 2041 gtgtgtcttctcttggagaaactccatctcctgtgtctctccacaccccgctccactc 2100
Db 2041 gtgtgtcttctcttggagaaactccatctcctgtgtctctccacaccccgctccactc 2100
QY 2101 ccccaactggaatgagcagctagactgagtgaggtcttcagagctcttcttcgtagag 2160
Db 2101 ccccaactggaatgagcagctagactgagtgaggtcttccagagctcttcttcgtagag 2160
QY 2161 tcggccccaatgggaactagtaactctctctcta 2196
Db 2161 tcggccccaatgggaactagtaactctctctcta 2196

RESULT 8
US-09-660-872-3
: Sequence 3, Application US/09660872
: GENERAL INFORMATION:
: APPLICANT: ROZEN, Rima
: APPLICANT: COLETTE, Philippe
: TITLE OF INVENTION: CDNA FOR HUMAN METHYLENETHETRAHYDROFOLATE
: TITLE OF INVENTION: REDUCTASE
: FILE REFERENCE: 04844/005004
: CURRENT APPLICATION NUMBER: US/09/660, 872
: PRIOR FILING DATE: 2000-09-13
: PRIOR APPLICATION NUMBER: GB 9410620.0
: PRIOR FILING DATE: 1994-05-26
: PRIOR APPLICATION NUMBER: US 08/738, 000
: PRIOR FILING DATE: 1997-02-12
: PRIOR APPLICATION NUMBER: US 09/258, 928
: PRIOR FILING DATE: 1999-03-01
: NUMBER OF SEQ ID NOS: 14
: SOFTWARE: FASTSEQ for Windows Version 4.0
: SEQ ID NO 3
: LENGTH: 2219
: TYPE: DNA
: ORGANISM: Homo sapiens
: FEATURE:
: NAME/KEY: CDS
: LOCATION: (13)...(1983)
US-09-660-872-3

Query Match 99.6%: Score 2186.6: DB 26: Length 2219;
Best Local Similarity 99.7%: Pred. No. 0;
Matches 2189: Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 aatccgagcagcatggtgaaagcagcagaggaagaaacagcagctcaacccctgttgag 60
Db 1 aatccgagcagcatggtgaaagcagcagaggaagaaacagcagctcaacccctgttgag 60

QY 61 ggcaatgccaagagtgagcagtgatagagcttccaaagatgttcgagatgttccacccgggc 120
Db 61 ggcaatgccaagagtgagcagtgatagagcttccaaagatgttcgagatgttccacccgggc 120
QY 121 ctggaacccctgaaagcagcatgagagactccggggaagaaatgaaagcagcagcttgaaatctgt 180
Db 121 ctggaacccctgaaagcagcatgagagactccggggaagaaatgaaagcagcagcttgaaatctgt 180
QY 181 gacaaagtgttctcccttgaaatcttccctccctcgaactgtctgagagagctgtcaatctc 240
Db 181 gacaaagtgttctcccttgaaatcttccctccctcgaactgtctgagagagctgtcaatctc 240
QY 241 atctcaagtttgacccagatgagcagcaggttgccccctcctacatgagtgatctgagac 300
Db 241 atctcaagtttgacccagatgagcagcaggttgccccctcctacatgagtgatctgagac 300
QY 301 ccaagcagtgacccctgtgtcagacaagagacacttccatgatgatctgcagacacgcgc 360
Db 301 ccaagcagtgacccctgtgtcagacaagagacacttccatgatgatctgcagacacgcgc 360
QY 361 gtgaactactgttgccctgagagacatccctgacatgactgtctgcgttcaagcgcctggag 420
Db 361 gtgaactactgttgccctgagagacatccctgacatgactgtctgcgttcaagcgcctggag 420
QY 421 gagatcagggccactctgcaacaagctlaagcagcttggtcgtgaggaacatcatgtgcgtg 480
Db 421 gagatcagggccactctgcaacaagctlaagcagcttggtcgtgaggaacatcatgtgcgtg 480
QY 481 cggggagagcccaatagtgagaccagtgaggaaagagagagagagagcttcaactaagcagtg 540
Db 481 cggggagagcccaatagtgagaccagtgaggaaagagagagagagagagcttcaactaagcagtg 540
QY 541 gacctgtgaaagcacaatccgaagtgagttgtgtactactgtgacatctgtgtgagcaggt 600
Db 541 gacctgtgaaagcacaatccgaagtgagttgtgtactactgtgacatctgtgtgagcaggt 600
QY 601 taaccaagagcacaaccccgaaagcagagagcttggagctgacactgaaagcacttgaagag 660
Db 601 taaccaagagcacaaccccgaaagcagagagcttggagctgacactgaaagcacttgaagag 660
QY 661 aaggtgtntcgggagcgagattatcatcatcagagagcttcttctgtgagctgacacatc 720
Db 661 aaggtgtntcgggagcgagattatcatcatcagagagcttcttctgtgagctgacacatc 720
QY 721 ttccgcttgtgaaagagatgacaccagatgagatgagatcttgcacacgctgcagagtgag 780
Db 721 ttccgcttgtgaaagagatgacaccagatgagatgagatcttgcacacgctgcagagtgag 780
QY 781 ttcccatcagaggtacacactccctcgtgcagctgtgtgaagctgttccaaagctggaggtg 840
Db 781 ttcccatcagaggtacacactccctcgtgcagctgtgtgaagctgttccaaagctggaggtg 840
QY 841 ccaagagagatcaagagcgtgatatgagcacaatcaaaaacaaagatgtgtgacacacac 900
Db 841 ccaagagagatcaagagcgtgatatgagcacaatcaaaaacaaagatgtgtgacacacac 900
QY 901 tatgtcagcagctgtgcgtgtgagcctgtgtccaaagagcttgcagcagtggtgtgtgca 960
Db 901 tatgtcagcagctgtgcgtgtgagcctgtgtccaaagagcttgcagcagtggtgtgtgca 960
QY 961 ggcctcaactctacacccctcaaccccgagatgagctgtacacaaaggtgtctgaagcgctg 1020
Db 961 ggcctcaactctacacccctcaaccccgagatgagctgtgtacacaaaggtgtctgaagcgctg 1020
QY 1021 gggatgtgacttgagagaccccaagcgctccctcactcgtcgtcagtgcccaaccccaag 1080
Db 1021 gggatgtgacttgagagaccccaagcgctccctcactcgtcgtcagtgcccaaccccaag 1080
QY 1081 cgcagagagagagatgataagctccatctctgggctcagacaaagaggtataatctac 1140
Db 1081 cgcagagagagagatgataagctccatcttctggcctcagacaaagaggtataatctac 1140
QY 1141 cgtaccagagagtgagagaggttccctaaagcgcgttgaggaaattcccttccctgcgc 1200

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Db 1141 cgtaccagagatgaggagactactactcttaccctgaaggaagtcctcccaaggaag 1260
QY 1201 ttctggagagctgaaggaactactactcttaccctgaaggaagtcctcccaaggaag 1260
Db 1201 ttctggagagctgaaggaactactactcttaccctgaaggaagtcctcccaaggaag 1260
QY 1261 ctgctgaagatgtgaggaggagagctgaagcaatgaagcaagtcctgaagtcctgtt 1320
Db 1261 ctgctgaagatgtgaggaggagagctgaagcaatgaagcaagtcctgaagtcctgtt 1320
QY 1321 ctttaacctctcgaggagagagcaaacccggaatggttcacaaatgagcttgcgcgcctgaac 1380
Db 1321 ctttaacctctcgaggagagagcaaacccggaatggttcacaaatgagcttgcgcgcctgaac 1380
QY 1381 gatgaagcccttgagcgtgaggaacagctctgaaggaagagctgctgaggaagtcctgaac 1440
Db 1381 gatgaagcccttgagcgtgaggaacagctctgaaggaagagctgctgaggaagtcctgaac 1440
QY 1441 caggagcctctccacacacacacacacacacacacacacacacacacacacacacacacac 1500
Db 1441 caggagcctctccacacacacacacacacacacacacacacacacacacacacacacacac 1500
QY 1501 atcgtgggctggggcccgagcgggggctatgctcttcacaggaagcctactagaagttttc 1560
Db 1501 atcgtgggctggggcccgagcgggggctatgctcttcacaggaagcctactagaagttttc 1560
QY 1561 acttcccgagagacagcggaggaacacttctgaagtgctgaaggaagtaagagctccgggtc 1620
Db 1561 acttcccgagagacagcggaggaacacttctgaagtgctgaaggaagtaagagctccgggtc 1620
QY 1621 aattacacacttgcataatgaggggtgaaataacacacacacacacacacacacacacacacac 1680
Db 1621 aattacacacttgcataatgaggggtgaaataacacacacacacacacacacacacacacacac 1680
QY 1681 aatgctgctcaacttgggggcatcttccctggggcgagagataccacagccacagtaagtt 1740
Db 1681 aatgctgctcaacttgggggcatcttccctggggcgagagataccacagccacagtaagtt 1740
QY 1741 ccgcctgaagcttcatgtctggaagagcgaagccttgcctctgagatgagtgagtgaggga 1800
Db 1741 ccgcctgaagcttcatgtctggaagagcgaagccttgcctctgagatgagtgagtgaggga 1800
QY 1801 aagctgtatgagagagagagtcctccgctccgacacacacacacacacacacacacacacacac 1860
Db 1801 aagctgtatgagagagagagtcctccgctccgacacacacacacacacacacacacacacacac 1860
QY 1861 ttctctgctcaacacttggtgacaaatgacttccacatgacacacacacacacacacacacacacacacac 1920
Db 1861 ttctctgctcaacacttggtgacaaatgacttccacatgacacacacacacacacacacacacacacacac 1920
QY 1921 gaagacacatgagagcttctcaacacagccacacacacacacacacacacacacacacacacacacacacac 1980
Db 1921 gaagacacatgagagcttctcaacacagccacacacacacacacacacacacacacacacacacacacacac 1980
QY 1981 tgaacctggtctctgagcgccttggtgagacacacacacacacacacacacacacacacacacacacacacac 2040
Db 1981 tgaacctggtctctgagcgccttggtgagacacacacacacacacacacacacacacacacacacacacacac 2040
QY 2041 gtgctgcttctcttggagacacacacacacacacacacacacacacacacacacacacacacacacacacacac 2100
Db 2041 gtgctgcttctcttggagacacacacacacacacacacacacacacacacacacacacacacacacacacacac 2100
QY 2101 ccccaactgacaaatgagcagctagactgagtgaggtcttcacagctcttctctgagacctgag 2160
Db 2101 ccccaactgacaaatgagcagctagactgagtgaggtcttcacagctcttctctgagacctgag 2160
QY 2161 tcggccccacatgaggaactagtaactctgtctca 2196
Db 2161 tcggccccacatgaggaactagtaactctgtctca 2196

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RESULT 9

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US-09-660-872A-3
; Sequence 3, Application US/09660872A
; GENERAL INFORMATION:
; APPLICANT: KOZEN, Rima
; APPLICANT: GOTTET, Philippe
; TITLE OF INVENTION: CDNA FOR HUMAN METHYLENETETRAHYDROFOLATE
; FILE REFERENCE: 04844/005004
; CURRENT APPLICATION NUMBER: US/09/660, 872A
; CURRENT FILING DATE: 2000-09-13
; PRIOR APPLICATION NUMBER: PCT/IB00/00442
; PRIOR FILING DATE: 2000-02-28
; PRIOR APPLICATION NUMBER: US 09/258, 928
; PRIOR FILING DATE: 1999-03-01
; PRIOR APPLICATION NUMBER: US 08/738, 000
; PRIOR FILING DATE: 1997-02-12
; PRIOR APPLICATION NUMBER: PCT/CA95/00314
; PRIOR FILING DATE: 1995-05-25
; PRIOR APPLICATION NUMBER: GB 9410620.0
; PRIOR FILING DATE: 1994-05-26
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 2219
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (13)...(1983)
; US-09-660-872A-3

Query Match 99.6%; Score 2186.6; DB 26; Length 2219;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 2189; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 aattccggagcctatgtgtgacgaagccagaggaagacagcctcaacccctgtgag 60
Db 1 aattccggagcctatgtgtgacgaagccagaggaagacagcctcaacccctgtgag 60
QY 61 ggcagtgccagagtgagcagtgagagctccaaagatgttcgagatgttccacccgggc 120
Db 61 ggcagtgccagagtgagcagtgagagctccaaagatgttcgagatgttccacccgggc 120
QY 121 ctggacccctggaagcagatgagagactccgggagagatgagcggcgttgaaatctgt 180
Db 121 ctggacccctggaagcagatgagagactccgggagagatgagcggcgttgaaatctgt 180
QY 181 gacaagtgcttccctgtgaattcttccctcctcgaactgtcgaagtgagcgtgcaatctc 240
Db 181 gacaagtgcttccctgtgaattcttccctcctcgaactgtcgaagtgagcgtgcaatctc 240
QY 241 atctcaaggtttgacccgagatgagcagagtggtgccccctcaatagacgtgacgtgcac 300
Db 241 atctcaaggtttgacccgagatgagcagagtggtgccccctcaatagacgtgacgtgcac 300
QY 301 ccagcagtgacccctggtctcagaagaagagacactctcctcatgatatgacagacagcc 360
Db 301 ccagcagtgacccctggtctcagaagaagagacactctcctcatgatatgacagacagcc 360
QY 361 gtgaactactgtgacctgagacacacacacacacacacacacacacacacacacacacacacac 420
Db 361 gtgaactactgtgacctgagacacacacacacacacacacacacacacacacacacacacacac 420
QY 421 gagatcaaggcgcacatctcacaagaactgaagcctgggctcgaagaaacatcatatgacctg 480
Db 421 gagatcaaggcgcacatctcacaagaactgaagcctgggctcgaagaaacatcatatgacctg 480
QY 481 cggggagacccaatagtgagcagagtgaggagagagagagagagagagagagagagagagagag 540
Db 481 cggggagacccaatagtgagcagagtgaggagagagagagagagagagagagagagagagagag 540
QY 541 gacctgtgagagcacatccgaagtgagtttggtgactactctgacacatctgtgtgagagtc 600

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Db	1141	cgtaaccagagatgtagacagatctccataacgacggttgaggacattccctctctccctgccc	1200
QY	1201	tttggagagcgtgaagagatactataccctctctacccgtgaagaagaatcccccagaagagag	1260
Db	1201	tttggagagcgtgaagagatactataccctctctacccgtgaagaagaatcccccagaagagag	1260
QY	1261	ctgctgaagatgtgaggagagagagctgtanacagtgaagacaagtgtcttmgaaactctgtct	1320
Db	1261	ctgctgaagatgtgaggagagagagctgtanacagtgaagacaagtgtcttmgaaactctgtct	1320
QY	1321	ctttaacctccggagagaaacaaacccggaaatgttcaacaagtgtactgtgcttccttggaac	1380
Db	1321	ctttaacctccggagagaaacaaacccggaaatgttcaacaagtgtactgtgcttccttggaac	1380
QY	1381	gatgagacccctgagcgtctgagacacagcctgtctgaagagagagctgtgctgaggtgaacgcgc	1440
Db	1381	gatgagacccctgagcgtctgagacacagcctgtctgaagagagagctgtgctgaggtgaacgcgc	1440
QY	1441	cagggacatccctccacatactcaacacacaccccaacatacacaacggaggaagccgctcccgacccc	1500
Db	1441	cagggacatccctccacatactcaacacacaccccaacatacacaacggaggaagccgctcccgacccc	1500
QY	1501	atggttggtctggggcccccaagcgggggtatgtctctcaagaagcctactatagaagtctttc	1560
Db	1501	atggttggtctggggcccccaagcgggggtatgtctctcaagaagcctactatagaagtctttc	1560
QY	1561	acttcccgagaaacagcggaaagacaattctctgacaagtgtcgaagaagatccagagctccgggtt	1620
Db	1561	acttcccgagaaacagcggaaagacaattctctgacaagtgtcgaagaagatccagagctccgggtt	1620
QY	1621	aattacaacctgttaaatgtgaagaggtgaaataacatacacaatgcctccctgaactgcagccg	1680
Db	1621	aattacaacctgttaaatgtgaagaggtgaaataacatacacaatgcctccctgaactgcagccg	1680
QY	1681	aatgtctgatactctggggacatctccctctggagagaaagatacatacagccacagctagatgagat	1740
Db	1681	aatgtctgatactctggggacatctccctctggagagaaagatacatacagccacagctagatgagat	1740
QY	1741	cccggtacaagttatgttcttgaaagaaagagaccttttcgctctgatagtacagctggaggga	1800
Db	1741	cccggtacaagttatgttcttgaaagaaagagaccttttcgctctgatagtacagctggaggga	1800
QY	1801	aagctgtatgaaagagagatcccccgtcccgagacaatacatacagctacatacagaacaataac	1860
Db	1801	aagctgtatgaaagagagatcccccgtcccgagacaatacatacagctacatacagaacaataac	1860
QY	1861	ttccctggtcaaacctgtgtagacaatgaaatctccactctgagacaatactgtcctgtgcagatgtag	1920
Db	1861	ttccctggtcaaacctgtgtagacaatgaaatctccactctgagacaatactgtcctgtgcagatgtag	1920
QY	1921	gaagaacaatatgagactctctcaacaagagcccaacaaatgacagagaaacaggaagcttcca	1980
Db	1921	gaagaacaatatgagactctctcaacaagagcccaacaaatgacagagaaacaggaagcttcca	1980
QY	1981	tgaacctgtgcctcgtgaagccctctgtcttgagagccaactcctgttcccgctctctctcca	2040
Db	1981	tgaacctgtgcctcgtgaagccctctgtcttgagagccaactcctgttcccgctctctctcca	2040
QY	2041	gtgcgtctctcttggaactccaactctctctctgctctctcccaaccccgctcccaactc	2100
Db	2101	ccccacatgacaatgagagatgaactagacatcgagcttcacaaagctctctctctgagactgag	2160
QY	2161	tcggccccacatgagaaactagatgactctctgtctca	2196
Db	2161	tcggccccacatgagaaactagatgactctctgtctca	2196


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; Sequence 1, Application US/09592595
; GENERAL INFORMATION:
; APPLICANT: ROZEN, Rima
; TITLE OF INVENTION: CDNA FOR HUMAN METHYLENETHETRAHYDROFOLATE
; FILE REFERENCE: 04844/005005
; CURRENT APPLICATION NUMBER: US/09/592,595
; CURRENT FILING DATE: 2000-06-12
; PRIOR APPLICATION NUMBER: US 09/258,928
; PRIOR FILING DATE: 1999-03-01
; PRIOR APPLICATION NUMBER: US 08/738,000
; PRIOR FILING DATE: 1997-02-12
; PRIOR APPLICATION NUMBER: PCT/CA95/00314
; PRIOR FILING DATE: 1995-05-25
; PRIOR APPLICATION NUMBER: GB 9410620.0
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 2220
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(1980)
US-09-592-595-1
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Query Match          99.6%; Score 2186.6; DB 22; Length 2220;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 2189; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
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QY 1 aatcccgagcgcatggtgagacgaagccagaggaacagacgacccctgcttgag 60
Db 1 aatccgagcgcatggtgagacgaagccagaggaacagacgacccctgcttgag 60
QY 61 ggcagtcgcaacgagctgagcagtgagagctccaaagatgttgcagatgttccacccgggc 120
Db 61 ggcagtcgcaacgagctgagcagtgagagctccaaagatgttgcagatgttccacccgggc 120
QY 121 ctggaacccctgagcgagcatgagagactccgggagagatgagcgagcttggaattcgtg 180
Db 121 ctggaacccctgagcgagcatgagagactccgggagagatgagcgagcttggaattcgtg 180
QY 181 gacagaggtttctccctcggaattcttcctcctcgaactgctgagggaggtgtcaattctc 240
Db 181 gacagaggtttctccctcggaattcttcctcctcgaactgctgagggaggtgtcaattctc 240
QY 241 atctcaaggtttgacgagatgagcaggtgagccctctacatagacgtgacctggcac 300
Db 241 atctcaaggtttgacgagatgagcaggtgagccctctacatagacgtgacctggcac 300
QY 301 ccagcaggtgacccctgctcagagagaagagacccctccatgatatcgccagcagcc 360
Db 301 ccagcaggtgacccctgctcagagagaagagacccctccatgatatcgccagcagcc 360
QY 361 gtgaactactgtgctgagcagacatctcctgacatgacccgtcgccgtcagcgtgag 420
Db 361 gtgaactactgtgctgagcagacatctcctgacatgacccgtcgccgtcagcgtgag 420
QY 421 ggaatacagcgcatctgacacaaagctaaagcagctgagcgtgaggaacatcatctgctg 480
Db 421 ggaatacagcgcatctgacacaaagctaaagcagctgagcgtgaggaacatcatctgctg 480
QY 481 cgggagagaccataagtgtagccagtgaggaagagagauagagcttcaactcgagctg 540
Db 481 cgggagagaccataagtgtagccagtgaggaagagagauagagcttcaactcgagctg 540
QY 541 gacctgtgaaagcacaatcogaagtgaattgtgtaactacttgacactctgtgtgagagt 600
Db 541 gacctgtgaaagcacaatcogaagtgaattgtgtaactacttgacactctgtgtgagagt 600
QY 601 taacccaagcgcaaccccggaagcagagagctttagagctgacactgaaagcacttgaaagag 660
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Db 601 taacccaagcgcaaccccggaagcagagagctttagagctgacactgaaagcacttgaaagag 660
QY 661 aaggtgntgcggagcgcatcttcatacagcagacttctcttgaagctgacacatc 720
Db 661 aaggtgntgcggagcgcatcttcatacagcagacttctcttgaagctgacacatc 720
QY 721 ttcgcttgtgaaagcagatgacacgacatgagcattcctccatcgctcccgagtc 780
Db 721 ttcgcttgtgaaagcagatgacacgacatgagcattcctccatcgctcccgagtc 780
QY 781 ttcccatcagagcgctacacacccctcgagcagctgtgaaactgttccaaagttagagtg 840
Db 781 ttcccatcagagcgctacacacccctcgagcagctgtgaaactgttccaaagttagagtg 840
QY 841 ccacagagatcaagaagcgtgattgagccaatcaaaagacagatgtgcataccgcaac 900
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QY 901 tatgcatcagagctgagcgtgagcgtgtgccaagagcttctgccaagtggctgtgtgcca 960
Db 901 tatgcatcagagctgagcgtgagcgtgtgccaagagcttctgccaagtggctgtgtgcca 960
QY 961 ggcctcactctctacacccctcaacccgagagatggtctacacagaggtgtctgaagcgctg 1020
Db 961 ggcctcactctctacacccctcaacccgagagatggtctacacagaggtgtctgaagcgctg 1020
QY 1021 gggatgtgacttgagagaccccaagcgctccctacacctcgctctagtgtcccaacgaag 1080
Db 1021 gggatgtgacttgagagaccccaagcgctccctacacctcgctctagtgtcccaacgaag 1080
QY 1081 cgcgagagagagatgtacgtcccatctctcgggctccacagaccaaagatctacac 1140
Db 1081 cgcgagagagagatgtacgtcccatctctcgggctccacagaccaaagatctacac 1140
QY 1141 cgtacccaagagctgtgagcagatctccctaaacggcgctgtggggcaattctctccctgccc 1200
Db 1141 cgtacccaagagctgtgagcagatctccctaaacggcgctgtggggcaattctctccctgccc 1200
QY 1201 ttgaggagcgtgaaagactatacctctctcactcgaagagcaagttccccaagagagag 1260
Db 1201 ttgaggagcgtgaaagactatacctctctcactcgaagagcaagttccccaagagagag 1260
QY 1261 ctgctgaagatgtgtggggagagcctgancagtgaaagcaagtgtcttgaagatcttctgt 1320
Db 1261 ctgctgaagatgtgtggggagagcctgancagtgaaagcaagtgtcttgaagatcttctgt 1320
QY 1321 cttaactctcgggagaaacccaacgggaatgtgtacaaagtgaattgctgctccctggaac 1380
Db 1321 cttaactctcgggagaaacccaacgggaatgtgtacaaagtgaattgctgctccctggaac 1380
QY 1381 gatgagccctctgagctgagacagcctctgtaagagagagcgctgctggcggtgaaacgcg 1440
Db 1381 gatgagccctctgagctgagacagcctctgtaagagagagcgctgctggcggtgaaacgcg 1440
QY 1441 caggagcatctctcaacatcaactcaagcccaacatcaacggggaagcgctcctcgacccc 1500
Db 1441 caggagcatctctcaacatcaactcaagcccaacatcaacggggaagcgctcctcgacccc 1500
QY 1501 atcgtgagctggggcccaacgggggtatgtctctcagaagagcgctctaaaggttttc 1560
Db 1501 atcgtgagctggggcccaacgggggtatgtctctcagaagagcgctctaaaggttttc 1560
QY 1561 acttcccgagagacagcggagacactctctgcaagtgtctgaagaggtacgagctccggtt 1620
Db 1561 acttcccgagagacagcggagacactctctgcaagtgtctgaagaggtacgagctccggtt 1620
QY 1621 aattacaacctgtcaatgtgaaaggttgaaatacacaatgccccctgaaactgacgagcg 1680
Db 1621 aattacaacctgtcaatgtgaaaggttgaaatacacaatgccccctgaaactgacgagcg 1680
QY 1681 aatgtgtcaactgtgggcatctcctctggcgagagatcatcagccacccgtaagtgtgt 1740
Db 1681 aatgtgtcaactgtgggcatctcctctggcgagagatcatcagccacccgtaagtgtgt 1740
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Db 1681 aatcgtcacttgaggacattccctggcgagagatcaccagccacgtatgagat 1740
QY 1741 ccgcgtcaactcattgtcttgaaagagagagccttgccctgtatgattgagcgttgaggaa 1800
Db 1741 ccgcgtcaactcattgtcttgaaagagagagccttgccctgtatgattgagcgttgaggaa 1800
QY 1801 aagctgtatagggaggaggtccgcgtccgcacatccatccagtatccatccagcgaactac 1860
Db 1801 aagctgtatagggaggaggtccgcgtccgcacatccatccagtatccatccagcgaactac 1860
QY 1861 ttccctgtcaacacctgtgtgaaacatgacttcccatctggaacaactgcctcttgaggtgtg 1920
Db 1861 ttccctgtcaacacctgtgtgaaacatgacttcccatctggaacaactgcctcttgaggtgtg 1920
QY 1921 gaagacacatgtgagccttctcaacagccacccagaatgcgagagagaagcgtgtccca 1980
Db 1921 gaagacacatgtgagccttctcaacagccacccagaatgcgagagagaagcgtgtccca 1980
QY 1981 tgacctgtcgtctcgaagccctgtgtgagagccactctctccgcgtcttctctccaca 2040
Db 1981 tgacctgtcgtctcgaagccctgtgtgagagccactctctccgcgtcttctctccaca 2040
QY 2041 gtgtgtcttctctgtggaaactccactctcctgtgtctctccaccccggtccctc 2100
Db 2041 gtgtgtcttctctgtggaaactccactctcctgtgtctctccaccccggtccctc 2100
QY 2101 ccccaactgacaatgtgagctagactgtgaggttccaggtcttctctgtgactgtag 2160
Db 2101 ccccaactgacaatgtgagctagactgtgaggttccaggtcttctctgtgactgtag 2160
QY 2161 tcggcccaacatgaggaaactagactctctgtctta 2196
Db 2161 tcggcccaacatgaggaaactagactctctgtctta 2196

RESULT 12
US-09-592-595A-1
Sequence 1, Application US/09592595A
GENERAL INFORMATION:
APPLICANT: ROZEN, Rima
TITLE OF INVENTION: CDNA FOR HUMAN METHYLENETHETRAHYDROFOLATE
FILE REFERENCE: 04844/005003
CURRENT APPLICATION NUMBER: US/09/592, 595A
CURRENT FILING DATE: 2000-06-12
PRIOR APPLICATION NUMBER: US 09/258, 928
PRIOR FILING DATE: 1999-03-01
PRIOR APPLICATION NUMBER: US 08/738, 000
PRIOR FILING DATE: 1997-02-12
PRIOR APPLICATION NUMBER: PCT/CA95/00314
PRIOR FILING DATE: 1995-05-25
PRIOR APPLICATION NUMBER: GB 9410620.0
NUMBER OF SEQ ID NOS: 18
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 1
LENGTH: 2220
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (1)...(1980)
US-09-592-595A-1

Query Match 99.6%; Score 2186.6; DB 22; Length 2220;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 2189; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 aattccgagcagcatgtgaacgaacccgagagaaacacagccttaaccctgtcttgag 60
Db 1 aattccgagcagcatgtgaacgaacccgagagaaacacagccttaaccctgtcttgag 60

QY 61 ggcagtgcagcagctgagcaagtgaagagctcccaagatatgttcgaagatgttccaccgccggc 120
Db 61 ggcagtgcagcagctgagcaagtgaagagctcccaagatatgttcgaagatgttccaccgccggc 120
QY 121 ctggaccctgaagcgacatgagagactcccgagagagatgagcgcgagatggaatctgt 180
Db 121 ctggaccctgaagcgacatgagagactcccgagagagatgagcgcgagatggaatctgt 180
QY 181 gacaagtggtttccctcggaattcttcctccctcggaactgtgaaaggagctgtcaatctc 240
Db 181 gacaagtggtttccctcggaattcttcctccctcggaactgtgaaaggagctgtcaatctc 240
QY 241 atctcaaggtttgaccggaatgagcaggtgtgccccctacataagcttgaaactgtgac 300
Db 241 atctcaaggtttgaccggaatgagcaggtgtgccccctacataagcttgaaactgtgac 300
QY 301 ccgacaggtgagacctgtgtcacaagagagagactctccatgatatgcgcagaccgc 360
Db 301 ccgacaggtgagacctgtgtcacaagagagagactctccatgatatgcgcagaccgc 360
QY 361 gtgaactactgtgacctgagagacatccctgacatgacctgtgcctgacgccttgag 420
Db 361 gtgaactactgtgacctgagagacatccctgacatgacctgtgcctgacgccttgag 420
QY 421 gagatcacgggccaatctgcacaagaactgaagcagctgggctctgaggaacatactagcgctg 480
Db 421 gagatcacgggccaatctgcacaagaactgaagcagctgggctctgaggaacatactagcgctg 480
QY 481 cgggagagaccacaataggtgacacagtgagagagagagagagaggtctcaactacagcagtg 540
Db 481 cgggagagaccacaataggtgacacagtgagagagagagagagaggtctcaactacagcagtg 540
QY 541 gacctgtgtgaagcacatcccgaaagtgaattgtgtgactaacttgaaactgtgtgagcagt 600
Db 541 gacctgtgtgaagcacatcccgaaagtgaattgtgtgactaacttgaaactgtgtgagcagt 600
QY 601 taaccccaagcgccaccccgaaagcaggtcttgaggtcgtgacctgaagcaattgaagag 660
Db 601 taaccccaagcgccaccccgaaagcaggtcttgaggtcgtgacctgaagcaattgaagag 660
QY 661 aaggtgtgtgagagcgccattcatalcaacagcagcttctcttgagagctgacacatc 720
Db 661 aaggtgtgtgagagcgccattcatalcaacagcagcttctcttgagagctgacacatc 720
QY 721 ttccgcttgtgtgaagcagtcacgcgaatgtgacactgtcccatctgtcccgagatc 780
Db 721 ttccgcttgtgtgaagcagtcacgcgaatgtgacactgtcccatctgtcccgagatc 780
QY 781 ttcccatccaagggtacacactcccttcggcagctgtgtgaagctgttcaagcttgaggtg 840
Db 781 ttcccatccaagggtacacactcccttcggcagctgtgtgaagctgttcaagcttgaggtg 840
QY 841 ccaacagagatcaagagcgtgtatgtgacccaatcaaaagacaagatgctgtccatccgcaac 900
Db 841 ccaacagagatcaagagcgtgtatgtgacccaatcaaaagacaagatgctgtccatccgcaac 900
QY 901 tatggcatcgagctgagcgtgtgagcctgtgccaagagccttctgccaagtggttgagcga 960
Db 901 tatggcatcgagctgagcgtgtgagcctgtgccaagagccttctgccaagtggttgagcga 960
QY 961 ggcctcaacttacaacctcaacccgagatgtgtctaaccaagaggtgtcgaagcgctgtg 1020
Db 961 ggcctcaacttacaacctcaacccgagatgtgtctaaccaagaggtgtcgaagcgctgtg 1020
QY 1021 gggatgtgacttgagagcccgagcggtccctacccctcagctcagtgccaccccaag 1080
Db 1021 gggatgtgacttgagagcccgagcggtccctacccctcagctcagtgccaccccaag 1080
QY 1081 cgcgagagagagatgtacgtcccatctctgtggctccacagcaagagattacatctac 1140
Db 1081 cgcgagagagagatgtacgtcccatctctgtggctccacagcaagagattacatctac 1140
QY 1141 cgtaccagaggtgagagaggttccctaaacggccgctgtgggcaattctcttccctgc 1200

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Db 1141 cgtaccagagatgtagcagatctccctaacgcccgtgaggcaattcctctccctgcgc 1200
Qy 1201 ttgtggagagctgaaggaactactctctctactgaaggaagcaagctccccaagagag 1260
Db 1201 ttgtggagagctgaaggaactactctctctactgaaggaagcaagctccccaagagag 1260
Qy 1261 ctgtctgaagatgtgtgggggagagctgtganaagatgaagcaagctgtctctgaagctt 1320
Db 1261 ctgtctgaagatgtgtgggggagagctgtganaagcaagctgtctctgaagcttctgtc 1320
Qy 1321 cttaacctctcggagagacccaacacggaaatggttacaagaatgtactgtctgcctgaa 1380
Db 1321 cttaacctctcggagagacccaacacggaaatggttacaagaatgtactgtctgcctgaa 1380
Qy 1381 gatgagcccttgctgctgagacacagctgtgaaagagagctgtcgtcggtgaacgcgc 1440
Db 1381 gatgagcccttgctgctgagacacagctgtgaaagagagctgtcgtcggtgaacgcgc 1440
Qy 1441 caggagatctctacatcaactcaacagcccaacatcaacggagagccgtctccgcagccc 1500
Db 1441 caggagatctctacatcaactcaacagcccaacatcaacggagagccgtctccgcagccc 1500
Qy 1501 atcgtggtcgtggggccccaacggggtatgtctctcagaagaagccctactagaagtttct 1560
Db 1501 atcgtggtcgtggggccccaacggggtatgtctctcagaagaagccctactagaagtttct 1560
Qy 1561 acttcccgcgagacagcgagacactctgtcaagtgctgaaagaagtaacagactccgggt 1620
Db 1561 acttcccgcgagacagcgagacactctgtcaagtgctgaaagaagtaacagactccgggt 1620
Qy 1621 aattacaacctgtcatatgtgaaggttgaaatacatcaactgacctggaactgcagcg 1680
Db 1621 aattacaacctgtcatatgtgaaggttgaaatacatcaactgacctggaactgcagcg 1680
Qy 1681 aatgtctcaacttggtgggcatctctccctgggcgagagatcatcacaagcccaagctgag 1740
Db 1681 aatgtctcaacttggtgggcatctctccctgggcgagagatcatcacaagcccaagctgag 1740
Qy 1741 cccgtcagactcaatgtctcggagagagagagagagagagagagagagagagagagagag 1800
Db 1741 cccgtcagactcaatgtctcggagagagagagagagagagagagagagagagagagagag 1800
Qy 1801 aagctgtatgagagagagagagagagagagagagagagagagagagagagagagagagag 1860
Db 1801 aagctgtatgagagagagagagagagagagagagagagagagagagagagagagagagag 1860
Qy 1861 ttcctgtcaacctgtgtgagacatgtactcccaatgtgagacactgtcctgtgcaggtgtg 1920
Db 1861 ttcctgtcaacctgtgtgagacatgtactcccaatgtgagacactgtcctgtgcaggtgtg 1920
Qy 1921 gaagacacatctgagagctcttcaacagagcccaacgaatgtgcgagagagagagagagag 1980
Db 1921 gaagacacatctgagagctcttcaacagagcccaacgaatgtgcgagagagagagagagag 1980
Qy 1981 tgaacctgtgctctgaacgctctgtgagacacactgtctgcgagagagagagagagag 2040
Db 1981 tgaacctgtgctctgaacgctctgtgagacacactgtctgcgagagagagagagagag 2040
Qy 2041 ggtcgtgctctctgtgagacactctctcctcgtctcctcctcctcctcctcctcctcctc 2100
Db 2041 ggtcgtgctctctgtgagacactctctcctcgtctcctcctcctcctcctcctcctcctc 2100
Qy 2101 ccccaactgaatgtgagagctgtgagagagagagagagagagagagagagagagagagagag 2160
Db 2101 ccccaactgaatgtgagagctgtgagagagagagagagagagagagagagagagagagagag 2160
Qy 2161 tcggcccaacatggaagagagagagagagagagagagagagagagagagagagagagagag 2196
Db 2161 tcggcccaacatggaagagagagagagagagagagagagagagagagagagagagagagag 2196

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RESULT 13

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US-09-660-872-1
; Sequence 1, Application US/09660872
; GENERAL INFORMATION:
; APPLICANT: KOZEN, Rima
; APPLICANT: GOYETTE, Philippe
; TITLE OF INVENTION: CDNA FOR HUMAN METHYLENETHETRAHYDROFOLATE
; TITLE OF INVENTION: REDUCTASE
; FILE REFERENCE: 0484/005004
; CURRENT APPLICATION NUMBER: US/09/660,872
; CURRENT FILING DATE: 2000-09-13
; PRIOR APPLICATION NUMBER: GB 9410620.0
; PRIOR FILING DATE: 1994-05-26
; PRIOR APPLICATION NUMBER: US 08/738,000
; PRIOR FILING DATE: 1997-02-12
; PRIOR APPLICATION NUMBER: US 09/258,928
; PRIOR FILING DATE: 1999-03-01
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 2220
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(1980)
; US-09-660-872-1

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Query Match 99.7%; Score 2186.6; DB 26; Length 2220;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 2189; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
Qy 1 aattccgagacatgtgtgaacgaagccagaggaagaaacagacccctcaacccctgttggag 60
Db 1 aattccgagacatgtgtgaacgaagccagaggaagaaacagacccctcaacccctgttggag 60
Qy 61 ggtcgtgagacagctgtgagagagagagagagagagagagagagagagagagagagagag 120
Db 61 ggtcgtgagacagctgtgagagagagagagagagagagagagagagagagagagagagag 120
Qy 121 ctgagacccctgagcgagatagagagagagagagagagagagagagagagagagagagag 180
Db 121 ctgagacccctgagcgagatagagagagagagagagagagagagagagagagagagagag 180
Qy 181 gacaaagtgtctccctgtgaatctctccctcctcctcctcctcctcctcctcctcctcctc 240
Db 181 gacaaagtgtctccctgtgaatctctccctcctcctcctcctcctcctcctcctcctcctc 240
Qy 241 atctcaaggttgagccgagatgagcagaggtgagccctctacatagagctgagacgtgcac 300
Db 241 atctcaaggttgagccgagatgagcagaggtgagccctctacatagagacgtgcacgtgcac 300
Qy 301 ccagcaggtgacccctgtgctcagaacagagagagagagagagagagagagagagagagagag 360
Db 301 ccagcaggtgacccctgtgctcagaacagagagagagagagagagagagagagagagagagag 360
Qy 361 gttgaactatgtgtgagcctgtgagacacatctgtcagatgagctgtcgtcagagagagag 420
Db 361 gttgaactatgtgtgagcctgtgagacacatctgtcagatgagctgtcgtcagagagagag 420
Qy 421 gagatcacgggacatctgacacaaagctaaagcagctgagagagagagagagagagagagag 480
Db 421 gagatcacgggacatctgacacaaagctaaagcagctgagagagagagagagagagagagag 480
Qy 481 cgggagagacccaatagtgagacagtgaggagagagagagagagagagagagagagagagagag 540
Db 481 cgggagagacccaatagtgagacagtgaggagagagagagagagagagagagagagagagagag 540
Qy 541 gacctgtgtgaagcacatcccgaaagtgaagtttggtgactactttgacatctgtgtgagaggt 600
Db 541 gacctgtgtgaagcacatcccgaaagtgaagtttggtgactactttgacatctgtgtgagaggt 600
Qy 601 taaccacaaggccaccccgaaagcagagagcttgagagcttgagacctgaaagcacttgagagag 660

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Db 601 taacccaaagccaccgaaagcaggtcttgaagccgaccctgaagcacttgaaggag 660
Oy 661 aaggtgintgcggagccgattctcatcaccagcagcttctcttgaggctgacacattc 720
Db 661 aaggtgtcgcggagccgattctcatcaccagcagcttctcttgaggctgacacattc 720
Oy 721 ttccgcttctgaagcagcaccgacatgagcattactgtcccatcgctcccgagatc 780
Db 721 ttccgcttctgaagcagcaccgacatgagcattactgtcccatcgctcccgagatc 780
Oy 781 ttcccatccagggtaccacccctcccgagctgtgaagctgtccagctgaggtg 840
Db 781 ttcccatccagggtaccacccctcccgagctgtgaagctgtccagctgaggtg 840
Oy 841 ccacagagatcaagagcgtgtatgagccaatcaaaagacagatgctccatccgcaac 900
Db 841 ccacagagatcaagagcgtgtatgagccaatcaaaagacagatgctccatccgcaac 900
Oy 901 tatgagcatgagctgagccgtgtgagccgtgtccaggagcttctgagcagtggtgagca 960
Db 901 tatgagcatgagctgagccgtgtgagccgtgtccaggagcttctgagcagtggtgagca 960
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Oy 1021 gggatgtgagctgagagaccccgagcgctccctacacccctgctgctcagtgctccacccaa 1080
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Oy 1081 cgcgcagagagaaatgtagctccatctctgagccctccagacaaagatctacatctac 1140
Db 1081 cgcgcagagagaaatgtagctccatctctgagccctccagacaaagatctacatctac 1140
Oy 1141 cgtaccacagagtgagagaggttcccttaacggcgctgggggaattccctccctgac 1200
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Oy 1201 ttggggagagctgaagagtaactactctctctacatgaagagcaagtcgcccaaggagag 1260
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Oy 1261 ctgctgaagaatgtgggggagagagcttgancaatgaagcaagtcgtcttgaatcttgtt 1320
Db 1261 ctgctgaagaatgtgggggagagagcttgancaatgaagcaagtcgtcttgaatcttgtt 1320
Oy 1321 cttacactctcgaggaaacccaacccggaatggtcacaaagtactgtcgtccctggagac 1380
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Oy 1381 gattgagccctctgagcgctgagagccagctgtctgaaggagagctgtcgggtgaacgc 1440
Db 1381 gattgagccctctgagcgctgagagccagctgtctgaaggagagctgtcgggtgaacgc 1440
Oy 1441 caggggcatcctacacatcaactacagcccaacatcaacgaggaacgcgtccctccgaccc 1500
Db 1441 caggggcatcctacacatcaactacagcccaacatcaacgaggaacgcgtccctccgaccc 1500
Oy 1501 atcgtgagctgagggcccgagcggtgctatgtctccagaagcctacttagagtttttc 1560
Db 1501 atcgtgagctgagggcccgagcggtgctatgtctccagaagcctacttagagtttttc 1560
Oy 1561 acttcccgagagacagcggaagcacttctgcaagtgcggaagaaatgaagactcccggtt 1620
Db 1561 acttcccgagagacagcggaagcacttctgcaagtgcggaagaaatgaagactcccggtt 1620
Oy 1621 aattacacactgttcaatgtgaaggttgaaaaacatcaccaatgccccctgaaactgacgcg 1680
Db 1621 aattacacactgttcaatgtgaaggttgaaaaacatcaccaatgccccctgaaactgacgcg 1680
Oy 1681 aatgtgtcacttggggagatttccctgaggagagatcacccgacccgtagtgat 1740
Db 1681 aatgtgtcacttggggagatttccctgaggagagatcacccgacccgtagtgat 1740
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Db 1681 aatgtgtcacttggggagatttccctgaggagagatcacccgacccgtagtgat 1740
Oy 1741 cccgtcacattcatgttctgaaagagacgagcgcttgcctgtgagattgaagcggtgggaa 1800
Db 1741 cccgtcacattcatgttctgaaagagacgagcgcttgcctgtgagattgaagcggtgggaa 1800
Oy 1801 aagctgtatgagagagatcccgctcccgacacatcatcagttacatcacgaactaac 1860
Db 1801 aagctgtatgagagagatcccgctcccgacacatcatcagttacatcacgaactaac 1860
Oy 1861 ttccgtgtaaacctgtgtgaacatgacttcccaactggaacactgctctgtgaggtg 1920
Db 1861 ttccgtgtaaacctgtgtgaacatgacttcccaactggaacactgctctgtgaggtg 1920
Oy 1921 gaaagacacattgagagcttctcaacagcccaacccaagaaatgcgagagaaacggaagctcca 1980
Db 1921 gaaagacacattgagagcttctcaacagcccaacccaagaaatgcgagagaaacggaagctcca 1980
Oy 1981 tgaccctgctcgtgagcccgctgagctgtgagacaaactcgtcccgcttctctccaca 2040
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Oy 2041 gtctgtctctcttgggaactcactctcctctgtctctccaccccgctcactc 2100
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Oy 2101 ccccaactgacaaatgacagctagagctgagagcttccagcttcccttcctgagacctgag 2160
Db 2101 ccccaactgacaaatgacagctagagctgagagcttccagcttcccttcctgagacctgag 2160
Oy 2161 tcggccccacatgagaaactagtaactctgtctcta 2196
Db 2161 tcggccccacatgagaaactagtaactctgtctcta 2196

RESULT 14
US-09-660-872A-1
; Sequence 1, Application US/09660872A
; GENERAL INFORMATION:
; APPLICANT: ROZEN, Rima
; APPLICANT: GOYETTE, Philippe
; TITLE OR INVENTION: CDNA FOR HUMAN METHYLENETHETRAHYDROFOLATE
; FILE REFERENCE: 04844/005004
; CURRENT APPLICATION NUMBER: US/09/660, 872A
; PRIOR FILING DATE: 2000-09-13
; PRIOR APPLICATION NUMBER: PCT/IB00/00442
; PRIOR FILING DATE: 2000-02-28
; PRIOR APPLICATION NUMBER: US 09/258, 928
; PRIOR FILING DATE: 1999-03-01
; PRIOR APPLICATION NUMBER: US 08/738, 000
; PRIOR FILING DATE: 1997-02-12
; PRIOR APPLICATION NUMBER: PCT/CA95/00314
; PRIOR FILING DATE: 1995-05-25
; PRIOR APPLICATION NUMBER: GB 9410620.0
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 2220
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(1980)
; US-09-660-872A-1

Query Match 99.6%; Score 2186.6; DB 26; Length 2220;
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QY 181 gacaatggtcttcccttgaaattcttccctccctgaaactgctgaaggagctgtcaatc 240
Db 181 gacaatggtcttcccttgaaattcttccctccctgaaactgctgaaggagctgtcaatc 240
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Sequence 1, Application US/09728910
GENERAL INFORMATION:
APPLICANT: Rozen, Rima
TITLE OF INVENTION: CDNA FOR HUMAN METHYLENTERETRAHYDROFOLATE
FILE REFERENCE: 04844/006001
CURRENT APPLICATION NUMBER: US/09/728,910
PRIOR FILING DATE: 2000-12-01
PRIORITY APPLICATION NUMBER: US 09/258,928
NUMBER OF SEQ ID NOS: 15
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 1
LENGTH: 2220
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (1)...(1980)
US-09-728-910-1

Query Match          99.6%; Score 2186.6; DB 29; Length 2220;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 2189; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

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Search completed: June 26, 2002, 18:37:35
Job time: 10587 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 26, 2002, 16:20:18 ; Search time 321.18 Seconds
(without alignments)
10443.366 Million cell updates/sec

Title: **SEQ1MOD**
Sequence: 2196
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IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1044500 seqs, 763706786 residues
Total number of hits satisfying chosen parameters: 2089000

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2188	99.6	2196	US-09-638-267-1	Sequence 1, Appl
2	2186.6	99.6	2219	US-09-931-795-3	Sequence 3, Appl
3	2186.6	99.6	2220	US-09-931-795-1	Sequence 1, Appl
4	2177.6	99.2	2187	US-09-371-347A-51	Sequence 51, Appl
5	305.2	13.9	1689	US-60-360-039-27188	Sequence 27188, A
6	237.8	10.8	1994	PCT-US02-10064-3	Sequence 3, Appl
7	194	8.8	1800	US-60-360-039-45612	Sequence 45612, A
8	194	8.8	3082	PCT-US02-10064-1	Sequence 1, Appl
9	184.6	8.4	1809	US-60-360-039-25804	Sequence 25804, A
10	110.6	5.0	112	PCT-US01-47593-21	Sequence 21, Appl
11	110.6	5.0	112	PCT-US01-47593-23	Sequence 23, Appl
12	77.6	3.5	323	US-09-975-254-15156	Sequence 15156, A
13	64.8	3.0	2031	US-60-360-039-26809	Sequence 26809, A
14	62.4	2.8	1923	US-09-975-254-20206	Sequence 20206, A
15	61.6	2.8	353	US-60-360-039-29215	Sequence 29215, A
16	50	2.3	1974	US-60-360-039-46191	Sequence 46191, A
17	49.4	2.2	1974	US-60-360-039-46191	Sequence 214, App
18	49	2.2	50	US-09-940-244-214	Sequence 214, App
19	48.2	2.2	2187	US-09-371-347A-51	Sequence 51, Appl
20	48.2	2.2	2219	US-09-931-795-3	Sequence 3, Appl
21	48.2	2.2	2220	US-09-931-795-1	Sequence 1, Appl
22	47.8	2.2	1089	US-09-540-209B-4276	Sequence 4276, App
23	47.8	2.2	2196	US-09-638-267-1	Sequence 1, Appl
24	47.4	2.2	50	US-09-940-244-215	Sequence 215, App
25	46	2.1	28882	US-10-158-844-140	Sequence 140, App
26	44.8	2.0	271	US-09-975-254-24417	Sequence 24417, A

27	44.4	2.0	278	5	US-09-540-210B-33036	Sequence 33036, A
28	43.6	2.0	1275	7	US-60-360-039-32228	Sequence 32228, A
29	43	2.0	376	7	US-60-360-039-43150	Sequence 43150, A
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31	42	1.9	63	1	PCT-US01-47593-24	Sequence 24, Appl
32	41.6	1.9	249	5	US-09-975-254-12486	Sequence 12486, A
33	40.8	1.9	245	5	US-09-975-254-19625	Sequence 19625, A
34	40.6	1.8	833	6	US-10-143-775-116	Sequence 43111, A
35	40.6	1.8	1743	7	US-60-360-039-43111	Sequence 43111, A
36	40.4	1.8	63	1	PCT-US01-47593-25	Sequence 25, Appl
37	40.4	1.8	200	5	US-09-540-210B-11178	Sequence 11178, A
38	40.4	1.8	3036	5	US-09-053-375B-1472	Sequence 1472, App
39	40.4	1.8	3036	5	US-09-442-384B-471	Sequence 471, App
40	39.8	1.8	1182	7	US-60-360-039-24447	Sequence 24447, A
41	39.8	1.8	5877	6	US-10-152-886-54	Sequence 54, Appl
42	39.6	1.8	1329	7	US-60-360-039-31633	Sequence 31633, A
43	39.4	1.8	594	6	US-10-123-155-10	Sequence 10, Appl
44	39.4	1.8	594	6	US-10-137-871-10	Sequence 10, Appl
45	39.4	1.8	594	6	US-10-141-761-10	Sequence 10, Appl

ALIGNMENTS

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RESULT 1
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; Sequence 1, Application US/09638267
; GENERAL INFORMATION:
; APPLICANT: Stanton, Jr., Vincent P.
; TITLE OF INVENTION: GENE SEQUENCE VARIANCES IN GENES RELATED
; TITLE OF INVENTION: TO FOLATE METABOLISM HAVING UTILITY IN
; FILE REFERENCE: 11926-092001
; CURRENT APPLICATION NUMBER: US/09/638,267
; CURRENT FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 09/596,033
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 09/357,743
; PRIOR FILING DATE: 1999-07-20
; PRIOR APPLICATION NUMBER: 09/357,024
; PRIOR FILING DATE: 1999-07-19
; PRIOR APPLICATION NUMBER: 60/093,484
; PRIOR FILING DATE: 1998-07-20
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 2196
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic construct
; NAME/KEY: misc-feature
; LOCATION: 1784
; FEATURE:
; OTHER INFORMATION: n = a or g
; NAME/KEY: misc-feature
; LOCATION: 464
; FEATURE:
; OTHER INFORMATION: n = g or t
; NAME/KEY: misc-feature
; LOCATION: 1289
; FEATURE:
; OTHER INFORMATION: n = c or a
; US-09-638-267-1

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Query Match 99.6%; Score 2188; DB 5; Length 2196;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 2191; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

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RESULT 3
; Sequence 1, Application US/0931795
; GENERAL INFORMATION:
; APPLICANT: ROZEN, Rama
; TITLE OF INVENTION: CDNA FOR HUMAN METHYLENETHETRAHYDROFOLATE
; TITLE OF INVENTION: REDUCTASE AND USES THEREOF
; FILE REFERENCE: 04844/005003
; CURRENT APPLICATION NUMBER: US/09/931,795
; PRIOR FILING DATE: 2001-08-16
; PRIOR APPLICATION NUMBER: US 09/592,595
; PRIOR FILING DATE: 2000-06-12
; PRIOR APPLICATION NUMBER: US 09/258,928
; PRIOR FILING DATE: 1999-03-01
; PRIOR APPLICATION NUMBER: US 08/738,000
; PRIOR FILING DATE: 1997-02-12
; PRIOR APPLICATION NUMBER: PCT/CA95/00314
; PRIOR FILING DATE: 1995-05-25
; PRIOR APPLICATION NUMBER: GB 9410620.0
; PRIOR FILING DATE: 1994-05-26
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 2220
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(1980)
US-09-931-795-1
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Query Match 99.6%; Score 2186.6; DB 5; Length 2220;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 2189; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

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Db	1981	tgaacctctcgctctgaaagcccttggttttgaggagcaacctgctccgctctctccctccaca	2040
Qy	2041	gtctgctctctctctgtggaactcaactctctctggtlctctccaccccgctctcaactc	2100
Db	2041	gtctgctctctctctgtggaactcaactctctctggtlctctccaccccgctctcaactc	2100

Query Match	Best Local Similarity	99.7%	Score 2177.6	DB 5	Length 2187	Matches 2180	Conservative	0	Mismatches	7	Indels	0	Gaps	0
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: Sequence 27188, Application US/60360039			
: GENERAL INFORMATION:			
: APPLICANT: Cao, Yongwei			
: APPLICANT: Chen, Xianfeng			
: APPLICANT: Goldman, Barry S.			
: APPLICANT: Hinkle, Gregory J.			
: APPLICANT: Slater, Steven C.			
: TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF			
: FILE REFERENCE: 38-10(52052)A			
: CURRENT APPLICATION NUMBER: US/60/360, 039			
: CURRENT FILING DATE: 2002-02-21			
: NUMBER OF SEQ ID NOS: 47374			
: SEQ ID NO 27188			
: LENGTH: 1689			
: TYPE: DNA			
: ORGANISM: Neurospora crassa			
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Best Local Similarity 53.0%; Pred. No. 6.4e-62;			
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RESULT      6
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; Sequence 3, Application PC/TUS0210064
; GENERAL INFORMATION:
; APPLICANT: Applimg, Dean R.
; APPLICANT: Hanson, Andrew D.
; APPLICANT: Raymond, Rhonda R.
; APPLICANT: Roje, Sanja
; TITLE OF INVENTION: Biosynthesis of S-Adenosyl Methionine in a Recombinant
; TITLE OF INVENTION: Yeast Strain
; FILE REFERENCE: 119927-2009
; CURRENT APPLICATION NUMBER: PCT/US02/10064
; CURRENT FILING DATE: 2002-03-29
; PRIOR APPLICATION NUMBER: 60/280,333
; PRIOR FILING DATE: 2001-03-30
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3
; LENGTH: 1994
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (63)..(1841)
; OTHER INFORMATION: DNA construct
PCT-US02-10064-3

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Query Match	10.8%;	Score 237.8;	DB 1;	Length 1994;
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QY 1735 gtgtagctcgcgtacatgattcttggaaagacgaagccttctgtagctgtagtagagcgg 1794
   |||||
Db 1653 gtgtagtcaagcaggttcaaaagctgtggaagaagcgaagcgtttagattgttgcagaagc 1712
QY 1795 tgggaaagcgtgtagaggaagatcccgctcccgcaacatcatcagtagcatccagac 1854
   |||||
Db 1713 tgggttaactgttgcacccaagaagatgagccctctagaagaattgtcgtgtagagtgaaagac 1772
QY 1855 aactactcctgtgtaacctgtgtgtagacatgactc 1890
   |||||
Db 1773 agctactattgtgtagcgttagtgtagacaacaattac 1808

```

```

RESULT 7
US-60-039-45612
; Sequence 45612, Application US/60360039
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Chen, Xianfeng
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE REFERENCE: 38-10(52052)A
; CURRENT APPLICATION NUMBER: US/60/360,039
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 45612
; LENGTH: 1800
; TYPE: DNA
; ORGANISM: Saccharomyces cerevisiae
US-60-360-039-45612

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Query Match      8.8%; Score 194; DB 7; Length 1800;
Best Local Similarity 48.7%; Pred. No. 6-9e-36;
Matches 854; Conservative 0; Mismatches 823; Indels 78; Gaps 9;

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QY 175 tctgtgtacgaagtggtcttcctcgtgaattcttcctcctcgtgaactgtctgagggagctgtc 234
DB 40 tctgtgtacgaagcccaacttcaatcgcagtaacttcgtccggaagactacaagaagtgtaacg 99
QY 235 aatctcaatcgaagtttgacgagatg---gcaacaggttgcccccttacaatagacgtg 291
DB 100 aactgtatgacgagatgagccggatgtaagaggtctcttggcccaatttatgtgacac 159
QY 292 aactgtgaccccaagagtgtaacctgtgtctcagacaagagaaacctctccatgatgcgc 351
DB 160 acctgtgaatcagagcggtgtgacggtgtgacacatctg-----tccacgaacttggt 210
QY 352 agcccccgtgtgaactactgtgacctgagagaccatctcgtacatgatgcgtgtgcgtacg 411
DB 211 ggcagacagcagatctgtgtctgtgtgttgaaacgtgcatagcaccttaactgtgacacatg 270
QY 412 cgcctgagagagatcagcggccatctgcacaagaactaagcagctggtcgtgagaaacatc 471
DB 271 cccatttcgatatgatacagacgctttagaaacgcttatacctcgggttgccagaacatc 330
QY 472 atgagcgtcggagagaccccaatagtgac-----agtggagaagaggaugagggc 525
DB 331 ctgagcgtctgagagagagatctctcctcagagacgcagaacaaactggaactccggtgaaagtgagc 390
QY 526 ttaactacagcagtgagacgtgtgagacacatccgaagtgagttgtgtgactacttgac 585
DB 391 ttccaagatgccaagagcttgatgaatgaatataccaagtaacagtgacgtgtgacattcgct 450
QY 586 atcgtgtgacaggttaaccccaagcgacacccgaaagcagagactttagagctgacgtg 645
DB 451 atcggcgctgcgggtcaccggagtgccatccggaagtggtgcttaacaaagagtgaaagct 510
QY 646 aagcacttgaaggaagtgatglnbg---ggagcgatttcaatcacaacgacgttctc 702
DB 511 gatctcgaatttgagcagaagatcgacggcgcgacgtcattacatcaactcagatggtt 570
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DB 751 gacgagtggtccgtgtatcgcgaactaactgtgtggaagatgtgtcaaaaattgtc 810
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DB 1051 gaattcccaacggtagatccgtgatgtctctcctcgtctcgttgactt---ggat 1107

QY 1219 tactaccttcttcaactgaagaagcaagtcgcccaagagagagctgtcgtgaagatgtgg999 1278
DB 1108 ctgtgtgtgtcaagcttgatcagatcagcaatcagcgaacaaatgtctcgaattatgttccacc 1167
QY 1279 gaggagctgancagtgaaagcaagtgtctcttgaagctcttgtcttcaactcgg999aa 1338
DB 1168 cctacttccatcaacagcagctcgtctctgtgtcatc-----1203
QY 1339 ccaaacggaaatgttccaaagatgactgtgtcgtccctggaaacgatagtgacccctggcggt 1398
DB 1204 ---aactaactgtaagaaactgtgaagtgttaccctcgtgagatgatacccatcaatgat 1260
QY 1399 gagaacagctgtcgtgaagagagagctgtcgtgggtgaaacgcgcagggactcctacacac 1458
DB 1261 gaataataatccatccaagaagcacttgatgagtgtgaacacgactctcatcatcata 1320
QY 1459 aactcaacggcccaacatcaacagaggaagcggtccctccgacccatcgtgtgtggggccc 1518
DB 1321 aacttcaacactcaagtaacagcgcataggtccaaatgacaacaaatcattcagttgtgg99acc 1380
QY 1519 agcggggtatgtcttccaaagcctactgaagattttcaattcccgcgagacagcg 1578
DB 1381 aagatgtgttaagttacaggaagcaabatatttggaatttatgtgtgccaaagataagtg 1440
QY 1579 gaagcacttctgcgaagtgtcgaagatgagctccgggttaattacacactgtcaat 1638
DB 1441 cccaagtgtatgacacacttgaacaaatgagttcttgacactcttcgcacatgcagct 1500
QY 1639 gtgaaggttgaaacatcaacacatgcccttgaactgacgcggaatgtctgtcattgg99 1698
DB 1501 caaggtgacccgtcgaatgaatcaatccagacacaccccaagttcaacgctgtgactgg99t 1560
QY 1699 atcttccctggcgagagatcaatccagccacgcgtaagtgtatccgtcaactatgtc 1758
DB 1561 atttcccgcgagaaatcttcaactcaactcattgtcggaacaaatctgtcttctgagc 1620
QY 1759 tggagagcagagcgcttgcctgttagatgagcgtgtgggaaagcgtttagagagag 1818
DB 1621 tggagagcagagcttcatcatcatcttgaatgaatggaacaaacatgaaataacatgac 1660
QY 1819 tcccggtcccgacc---atcatcagttacatccagcaacactctcctgtgtgaactgt 1875
DB 1681 aaacgcagatgtcccaattcatcagtccttgattgacgtattgactgtgtgcaatatt 1740
QY 1876 gtgagcaatgactc 1890
DB 1741 gtgacaaatgactac 1755

RESULT 8
PCT-US02-10064-1
Sequence 1, Application PC/TUS0210064
GENERAL INFORMATION:
APPLICANT: Appling, Dean R.
APPLICANT: Hanson, Andrew D.
APPLICANT: Raymond, Rhonda R.
APPLICANT: Roje, Sanja
TITLE OF INVENTION: Biosynthesis of S-Adenosyl Methionine in a Recombinant
TITLE OF INVENTION: Yeast Strain
FILE REFERENCE: 119927-2009
CURRENT APPLICATION NUMBER: PCT/TUS02/10064
PRIOR FILING DATE: 2002-03-29
PRIOR APPLICATION NUMBER: 60/280,333
NUMBER OF SEQ ID NOS: 13
SOFTWARE: PatentIn version 3.0
SEQ ID NO 1
LENGTH: 3082
TYPE: DNA
ORGANISM: Saccharomyces cerevisiae
FEATURE:
NAME/KEY: CDS
LOCATION: (826)..(2625)

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OM nucleic - nucleic search, using sw model

Run on: June 26, 2002, 14:29:33 ; Search time 2329.2 Seconds
(Without alignments)
12725.104 Million cell updates/sec

Title: SEQMOD
Perfect score: 2196
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Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 13736207 seqs, 6748477542 residues

Total number of hits satisfying chosen parameters: 27472414

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

EST:*
1: em_estha:*
2: em_esthum:*
3: em_estlin:*
4: em_estnu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_hic:*
9: gb_estl:*
10: gb_estl2:*
11: gb_hic:*
12: gb_gss:*
13: em_gss_hum:*
14: em_gss_huv:*
15: em_gss_pln:*
16: em_gss_vrt:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	781	35.6	900	10	BG675748
2	542.2	24.7	556	10	BM310814
3	485.8	22.1	563	9	AU129663
4	466.8	21.3	654	9	BB617073
5	458.6	20.9	507	9	AI262190
6	446.4	20.3	556	10	BG384323
7	439.6	20.0	925	10	BI430422
8	434.4	19.8	774	9	AU169401
9	433.8	19.8	537	9	AM050775
10	358	16.3	457	10	BF654483
11	354.4	16.1	388	10	BF930775
12	352.4	16.0	400	10	BF934146
13	332	15.1	549	10	BM089718
14	321.8	14.7	499	9	AA183742
15	320.6	14.6	550	10	BE753120
16	311.4	14.2	650	10	BJ097085
17	309.4	14.1	614	10	BJ070955

18	308.2	14.0	572	9	AL647166
19	305.4	13.9	582	10	BJ069591
20	299.8	13.7	587	9	BE131889
21	295.2	13.4	560	10	BI066086
22	294.4	13.4	580	10	AJ393018
23	292.4	13.3	512	10	BM494723
24	281.8	12.8	335	9	AM436969
25	276.2	12.6	523	10	BJ066114
26	275	12.5	336	9	AM658667
27	273.6	12.5	461	10	BG979786
28	267.8	12.2	336	10	BF706718
29	266	12.1	309	9	AM636737
30	265.4	12.1	286	9	AA340811
31	262	11.9	488	9	BE190101
32	247.4	11.3	450	9	AM645737
33	224.6	10.2	469	10	BI849423
34	223.8	10.2	269	9	AM484848
35	219.8	10.0	223	10	BE244583
36	211.2	9.6	472	10	BG835531
37	209	9.5	437	9	BB850869
38	197.2	9.0	666	10	BJ100073
39	184.4	8.4	249	9	AM478874
40	165.4	7.5	587	10	BJ125503
41	162.8	7.4	966	10	BG745802
42	160.6	7.3	603	9	AU204758
43	157.4	7.2	615	10	BJ108206
44	155.4	7.1	411	9	AU241885

ALIGNMENTS

RESULT 1
LOCUS BG675748 900 bp mRNA
DEFINITION BG675748 602621974F1 NCI_CGAP_Skn4 Homo sapiens cDNA clone IMAGE:4746955 5', mRNA sequence.
ACCESSION BG675748
VERSION BG675748.1 GI:13907144
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 900)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strauberg, Ph.D.
Email: cgabs-remail.nih.gov
Tissue Procurement: James Cleaver, M.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at:
http://image.llnl.gov
Plate: LLM10596 row: c column: 20
High quality sequence stop: 894.
Location/Qualifiers
1. 900
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:4746955"
/clone_1lb="NCI_CGAP_Skn4"
/tissue_type="squamous cell carcinoma"
/lab_host="DH10B (TI phage-resistant)"
/note="Organ: skin; Vector: pCMV-SPORT6; Site_1: NotI; Site_2: SalI; Cloned unidirectionally. Primer: Oligo dr.
Average insert size 1.5kb. Library constructed by Life Technologies. Note: This is a NCI_CGAP Library."

BASE COUNT 198 a 269 c 247 g 186 t

ORIGIN

Query Match 35.6%; Score 781; DB 10; Length 900;
 Best Local Similarity 96.1%; Pred. No. 9.2e-161;
 Matches 799; Conservative 0; Mismatches 32; Indels 0; Gaps 0;

OY 1234 ctgaagagcaagtcctcccaagagagagctgctgaagatgtgggggagagagctgancagt 1293
 Db 37 CCGCTGACCAAGTCCCGCCAGAGAGAGCTGTAAGATGTGGGGGAGAGAGCTGACAGT 96
 OY 1294 gaagaaatgctctgnaagttcttcttaacctctcgagagaaacaaacaggaatgt 1353
 Db 97 GAGGAAATGCTTTGAAAGCTTTGTTTCACTTCGCGAGAGAACCAACCGGAATGT 156
 OY 1354 cacaagtgaattgcttgcctcgagagagagagagagagagagagagagagagagctg 1413
 Db 157 CACAAGAGACTTGCCTGCGCCCTGAGAGAGATGAGCCCTGGCGCTGAGACAGAGCTGCTG 216
 OY 1414 aaggaagagctgctgag 1473
 Db 217 AAGGAGAGAGCTGCTGCGGGTGAACCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 276
 OY 1474 atcaacgag 1533
 Db 277 ATCAACGAG 336
 OY 1534 ttccagaag 1593
 Db 337 TTCAG 396
 OY 1594 gtgctgaag 1653
 Db 397 GTGCTGAG 456
 OY 1654 atcaacag 1713
 Db 457 ATGACCAATGAG 516
 OY 1714 gaagatcaag 1773
 Db 517 GAGATATGAG 576
 OY 1774 ttgacctgag 1833
 Db 577 TTTGCCCTGTGATTGAG 636
 OY 1834 atcatcag 1893
 Db 637 ATGATCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 696
 OY 1894 ctgagacag 1953
 Db 697 CTGAGACAG 756
 OY 1954 cagagatgag 2013
 Db 757 CAGAAATGAG 816
 OY 2014 actctgtgcag 2064
 Db 817 ACTCTGTGCTCCCGCTTCT 867

RESULT 2
 BM310814 556 bp mRNA linear EST 03-JAN-2002
 LOCUS 1948H09.Y1 HR85 islet Homo sapiens cDNA 5' similar to SW:WTHR_HUMAN
 DEFINITION
 ACCESSION BM310814
 VERSION 1
 KEYWORDS EST, human.
 SOURCE

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE

1 (bases 1 to 556)
 Melton, D., Brown, J., Kenty, G., Permut, A., Lee, C., Kaestner, K.,
 Lemishka, I., Sceane, M., Brestelli, J., Gradwohl, G., Clifton, S.,
 Hillier, L., Maira, M., Pape, D., Wylie, T., Martin, J., Blistein, A.,
 Schmitt, A., Theising, B., Rittler, E., Ronko, I., Bennett, J., Cardenas,
 M., Gibbons, M., McCann, R., Cole, R., Tsagarelis, R., Williams, T.,
 Jackson, Y., and Bowers, Y.
 Endocrine Pancreas Consortium
 Unpublished (2000)
 Other-ESTs: 1948H09.x1
 Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue
 Endocrine Pancreas Consortium
 Harvard University, Howard Hughes Medical Institute
 Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,
 MA 02138
 Tel: 617-495-1812
 Fax: 617-495-8557
 Email: dmelton@biomph.harvard.edu
 Library was constructed by Dr. Hiroshi Inoue DNA sequencing by:
 Washington University Genome Sequencing Center For information on
 obtaining a clone please contact: Dr. Hiroshi Inoue
 (hinoue@im.wustl.edu)
 Seq primer: -40RP from Gibco
 High quality sequence stop: 429.

FEATURES

source
 Location/Qualifiers
 1..556
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone_lib="HR85 islet"
 /rissue_type="Purified pancreatic islet"
 /lab_host="DH10B"
 /note="Organ: Pancreas; Vector: pBluescript SK(-); Site_1:
 NotI; Site_2: XhoI; cDNA made by oligo-dT priming.
 Size-selected on agarose gel. Average insert size ~1kb. 5'
 XhoI site was destroyed after directional cloning.
 Amplified once. Contact information: Hiroshi Inoue, MD,
 Metabolism Div. (Alan Permut Lab), Washington University
 School of Medicine, Box 8127, 660 South Euclid Ave., St.
 Louis, MO 63110, E-mail: hinoue@imgate.wustl.edu, Tel:
 314-362-1916, Fax: 314-747-2692."

BASE COUNT 134 a 156 c 173 g 93 t
 ORIGIN

Query Match 24.7%; Score 542.2; DB 10; Length 556;
 Best Local Similarity 99.5%; Pred. No. 1.7e-108;
 Matches 544; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 9 acccatgtgaacgaagcag 68
 Db 10 AGCCATGTAAG 69
 OY 69 cagcagatgag 128
 Db 70 CAGCAGATGAG 129
 OY 129 tgagcggagatgag 188
 Db 130 CGAGCGCATGAG 189
 OY 189 gtctccctggaattctccctccctcgagagagagagagagagagagagagagagagagag 248
 Db 190 GTTCTCCCTGGAATTTCTCCCTCGAAGCTCTAGAGAGAGAGAGAGAGAGAGAGAGAG 249
 OY 249 gtttagcag 308
 Db 250 GTTTAGCGGATGAG 309
 OY 309 tgacctggtcagacag 368

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Db      310  TGACCTGCTCAGACAGAGAGACCTCCTCCATGATGATGCGCAGACACCGCCGTGAACCTA 369
QY      369  ctgtgacctggaagaccatctctgcacatgacctgtgcgttaagcgctggagggagatcac 428
Db      370  CTGTGGCTGTGAGACCACTCTGCACTAGCACTGCTGCGTGAAGCGCTGGAGGAGATCAC 429
QY      429  gggccatctgcacaaagctaagcagctggcgcttgaggaaacatactatgctgcggggaggaa 488
Db      430  GGGCATCTGCTGACAAAGACTAAGCAGCTGGCGCTGAAGAACATCATGGCGCTGGCGGGAGAA 489
QY      489  cccaatagtgagaccagtgaggaaagagagagagagcttaactacagcagtgagcttgt 548
Db      490  CCCAATAGGTGACCAAGTGGAGAGAGAGAGAGAGGCTTCACATCACTGACGTGAGCTGCTGT 549
QY      549  gaagcac 555
Db      550  GAAGCAC 556

RESULT 3
LOCUS   AUI29663
DEFINITION AUI29663 NT2RP2 Homo sapiens cDNA clone NT2RP2005995 5', mRNA
ACCESSION AUI29663
VERSION   AUI29663.1 GI:10990017
KEYWORDS  EST.
SOURCE    human.
ORGANISM  Homo sapiens
           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
REFERENCE 1 (bases 1 to 563)
AUTHORS   Ota,T., Nishikawa,T., Suzuki,Y., Ishii,S., Saito,K., Kawai,Y.,
           Yamamoto,J., Makatsuta,A., Nakamura,Y., Nagai,T., Sugano,S. and
           Isogai,T.
TITLE      HRI human cDNA project
JOURNAL   Unpublished (2000)
COMMENT   Contact: Takao Isogai
           Genomics Laboratory
           Helix Research Institute
           1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
           Tel: 81-438-52-3951
           Fax: 81-438-52-3952
           Email: genomics@hri.co.jp
           HRI human cDNA project; 5'- & 3'-end one pass sequencing; Helix
           Research Institute; cDNA library construction; Department of
           Virology, Institute of Medical Science, University of Tokyo, and
           Helix Research Institute.
FEATURES
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                  location/Qualifiers
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                  /clone="NT2RP2005995"
                  /clone_1lb="NT2RP2"
                  /cell_type="teratocarcinoma"
                  /cell_line="NT2"
                  /note="Vector: pME18SFL3; mRNA from NT2 neuronal precursor
                  cells after 2-weeks retinoic acid (RA) induction"
BASE COUNT      130 a 160 c 175 g 95 t
ORIGIN
Query Match 22.1%; Score 485.8; DB 9; Length 563;
Best Local Similarity 98.8%; Pred. No. 3.8e-96;
Matches 498; Conservative 0; Mismatches 5; Indels 1; Gaps 1;

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QY      129  tgaagcgatgagagactccggagagaatgagcgcgctattggatctgtgacaagt 188
Db      181  CGAGCGCATGAGAGACTCCGGAGAGATGAGCGCGGATTTGGAAATCTGTGACAAATG 240
QY      189  gtccctcctggaattctccctccctcgcgaactgctgaaggagctgcaatctcatcacaag 248
Db      241  GTTCCTCCTGGAATCTTCCCTCCCTCGAACTGCTGAGGAGAGCTGTCATTCATCTCAAG 300
QY      249  gttgaccggaatgagcagaggttgccccctcctaataagacgtgacgtgacccaagcagg 308
Db      301  GTTTGACCCGATGCGACAGAGGTGGCCCCCTCTACATTAACGTGACCTGGACCCAGCAGG 360
QY      309  tgaccctggtccagacaagagagactctctcatalatgctgcgaacagcgctgaaacta 368
Db      361  TGACCTGTGCTCAGACAAAGAGACCTCTCCATGATGATGCGCACACCGCGGTGAACCTA 420
QY      369  ctgtgacctgagagaccatctgcacatgacctgtgcctgcagcgctctgaggaagatcac 428
Db      421  CTGTGGCTGTGAGACCACTCTGCACTAGCACTGCTGCGCTGACGCGCTGGAGAGATCAC 480
QY      429  gggccatctgcacaaagctaagcagctggcgcttgaggaaacatactatgctgcggggaggaa 488
Db      481  GGGCATCTGCAAAAGCTAAGCAGCTGGCGCTGAANAAATCATCATGCGCTGGCGGGAGANA 540
QY      489  cccaatagtgagcagctgagaga 512
Db      541  -CCAATAGTGAACCAAGTGGAGANA 563

RESULT 4
LOCUS   BB617073
DEFINITION BB617073 RIKEN full-length enriched, adult male testis Mus musculus
ACCESSION BB617073
VERSION   BB617073.1 GI:15396258
KEYWORDS  EST.
SOURCE    house mouse.
ORGANISM  Mus musculus
           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
REFERENCE 1 (bases 1 to 654)
AUTHORS   Arakawa,T., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A.,
           Hiramoto,K., Horii,F., Ishii,Y., Ito,M., Kawai,J., Konno,H., Kouda
           , M., Koyra,S., Matsuyama,T., Miyazaki,A., Nomura,K., Ohno,M., Sasaki
           Okazaki,Y., Okido,T., Saito,R., Sakai,C., Sakai,K., Sano,H., Sasaki
           , D., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Suzuki,H.,
           Tagami,M., Tagawa,A., Takahashi,F., Takeda,Y., Tanaka,T., Toya,T.,
           Muramatsu,M. and Hayashizaki,Y.
           RIKEN Mouse ESTs (Arakawa,T., et al. 2001)
           Unpublished (2001)
           Contact: Yoshitake Hayashizaki
           Laboratory for Genome Exploration Research Group, RIKEN Genomic
           Sciences Center(GSC), Yokohama Institute
           The Institute of Physical and Chemical Research (RIKEN)
           1-7-22 Suenho-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
           Tel: 81-45-503-9222
           Fax: 81-45-503-9216
           Email: genome-res@sc.riken.go.jp,
           URL:http://genome.gsc.riken.go.jp/
           Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh
           , M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
           Normalization and subtraction of cap-trapper-selected cDNAs to
           prepare full-length cDNA libraries for rapid discovery of new
           genes. Genome Res. 10 (10), 1617-1630 (2000)
           wagi,K., Fujiwara,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,
           Wataniki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsunura
           , S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kita,A. and
           Hayashizaki,Y.
           RIKEN integrated sequence analysis (RISA) system--384-format
           sequencing pipeline with 384 multicapillary sequencer. Genome Res.
           10 (11), 1757-1771 (2000)

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Db	507	TCGGCATCTTCCTCGGCAAGAGATCATCAAGCCACCGTAGTGATCCCGTCACTTC	448
QY	1753	atgtcttgaaagaaagcaggcctttgccttgtatgattagcagtggtgggaaagcgtatag	1812
Db	447	ATGTTCTTGAAAGACAGACAGCCCTTTGGCCCTGTGTGATTGAGCCGGTGGGAAAGCGTATGAG	388
QY	1813	gaagagctcccgctcccgcaacatcaccc-agaatcatcaacagcaactactctt-gttca	1870
Db	387	MAGGAGATCCCGCTCCCGCACATCATCATCAAGTATCATCACGACCACTTCTCTGGAGTCA	328
QY	1871	acctgtgtgacaatgactctccactcacttgagaaactgctcctctgtcagagtggtggaagacat	1930
Db	327	ACCTGTGTGACATGACTCTCCACTGTGACACACTGCCCTCTGTGCAGGTGTGGAAGACAT	268
QY	1931	tggagcttctcaagagggccaccagaatgagagagaaacggaagctcctacagactctg	1990
Db	267	TGGAGCTTCTCAACAGAGCCACCCAGAAATGACAGAAAGAGAGGCTCATATACCTGTGG	208
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Db	207	TCTGTACGCGCTTGCGTTGGAGGACACTCGTCCCGCTTCCGCTCCTCAAGTGTGCTTC	148
QY	2051	tttttggaactcactctcctctctgtctctctccaccgccgcctcaactccccactga	2110
Db	147	TCTTGGGAAGCTCACCTCTCTTCTGTCCTCCACCCCGGCTCCACTCCCGCACCTGA	88
QY	2111	caatgacagctagactgagtgtaggcttcacagctccttcctgactgagtgagccac	2170
Db	87	CAATGGCAGCTAGACTGAGGTGAGGCTTCCAGGCTCTTCTGTGACTAGTGGCCCCAC	28
QY	2171	atgggaacctagactctctgctcta	2196
Db	27	ATGGAACTACTACTCTCTGCTTA	2
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DEFINITION	303363 MAMC 1P1G Sus scrofa	CDNA 5', mRNA sequence.	
ACCESSION	BG384323		
VERSION	BG384323.1	GI:13308795	
KEYWORDS	EST.		
SOURCE	pig.		
ORGANISM	Sus scrofa		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
AUTHORS	1 (bases 1 to 556)		
	Fahrenkrug,S.C., Freking,B.A., Rohrer,G.A., Smith,T.P.L., Casas,E.,		
	Stone,R.T., Heaton,M.P., Grosse,W.M., Bennett,G.A., Laegreid,W.W.		
	and Keeler,J.W.		
TITLE	Design and use of two pooled tissue normalized cDNA libraries for		
JOURNAL	EST discovery in swine		
COMMENT	Unpublished (2000)		
	Contact: Smith TPL		
	USDA, ARS, U.S. Meat Animal Research Center		
	PO Box 166, Clay Center, NE 68933-0166, USA		
	Tel: 402 762 4366		
	Fax: 402 762 4390		
	Email: smiththemail.marc.usda.gov		
	Single pass sequencing. Bases called and alt. trimmed with phred		
	v0.980904.e. Vector identified by cross_match with the -m1nscore 18		
	and -m1match 12 options.		
	PCR primers		
	FORWARD: AGGAACAGCTATGACCAT		
	BACKWARD: GTTTTCCAGTCACGACG		
	Plate: 90 row: 0 column: 22		
	Seq primer: ATTTAGGTGACACTAATG.		
	Location/Qualifiers		
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source	/db_xref="taxon:9823"		
	/clone_lib="MAMC 1P1G"		

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Db	1	ACGGGCTACTCTGCACAAAGGCCAAAGCGGTGGGCTGA-AAACATCTTGGCGCTGAGAGGA	59	
QY	487	gacctcatgtgtgacccagtggtggaaggggaagggaggggttcaactacgcatgtgactg	546	
Db	60	GACCCCTGTGTGTGACCAAGTGGGAAGAGGAGGAAGGAGGCTTACGCTACCTCCACAACTTG	119	
QY	547	gtcaaacacatccgaagtgatgtttgtgtactactttgacatctgtgtgtgcaagttacccc	606	
Db	120	GTGAAGCACAATCCGACGCGAGTTTGGTGTACTTCTGACGTCTGTGTGTGACAGTTAACCC	179	
QY	607	aaagggcccccgaagcaggaagctttgaagcttgaaccttgaagcacttgaagagaagtg	666	
Db	180	AAAGGCCACCCCGACGACGAGAGCTTGGAGCCGACCTGAACACCTGTAAGAGAAAGTG	239	
QY	667	tntgtgggggcccggatattatcatcaagcagctttcttttgaagctgtgacatctctgcg	726	
Db	240	GGCGGAGGAGCCGACTCTTCATCACCCAGCTTTCTTGGAGGCTGATACGTTCTTCCGC	299	
QY	727	tttgtgaagcagtcagccagacatgggacatcttgaccctcgtcccggaatcttccc	786	
Db	300	TTCCTTGAAGGCTTGTCTCCGAGATGGGATACACTGCCCCATCTCCCGGACATCTTCCC	359	
QY	787	atccagggctacactccctctgcgcagcttgtgaagctgtgtccaaagctggaagtgccaa	846	
Db	360	ATCCAGGGCTACACACTCCCTCCGGAGCTGTAAGCTGTCCAAAGCTGAGAGTGGCGAG	419	
QY	847	ggagatcaaggaagtgatgttgaagccaatcaagaacacagatgtgtccatccgcaactatgc	906	
Db	420	CAGATCAAGGAAGTATCGAGCCCATCAAAAGCAATGAGCGCCCATCCGCAACTATGTC	479	
QY	907	atcggcgtcggccgttagcctgtgcaggaagcttctgcgcagtggtgtgtgcagagctc	966	
Db	480	ATCGAGCAGCGCTGTGAGCTTGTGCCAGAGACTTGTGCCAGTGGCTGTGTGGCGGCTC	539	
QY	967	cactctctacaccctcaa	983	
Db	540	CACCTCTATACCTCAA	556	
RESULT 7				
LOCUS	B1430422	925 bp	linear	EST 16-AUG-2001
DEFINITION	UMN39807 Canine Brain cDNA library canine familiaris cDNA 5' similar to Human 5,10 methylentetrahydrofolate reductase (MADPH), mRNA			
ACCESSION	B1430422			
VERSION	B1430422.1	GI:15207654		
KEYWORDS	EST.			
SOURCE	dog.			
ORGANISM	Canis familiaris			
REFERENCE	Eukaryota; Metazoa; Chordata; Cranialta; Vertebrata; Euteleostomi; Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.			
AUTHORS	Robertson,M.C., Hendrickson,J.A., Hoffmann,D.E., Flickinger,G.H., Rutherford,M.S. and Mickelson,J.R.			
TITLE	University of Minnesota Canine Brain EST Project			
JOURNAL	Unpublished (2001)			
COMMENT	Contact: Mickelson, J.R.			


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Qy 1216 gactactacctcttctactcgaagcaagtcctcccaaggaagagctgctgaagatg 1275
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Db 541 GACATTAACCTTTCTTCTTAAGACCAATCATCGAAAGAGCTTTCTTCAAGATGG 600
Qy 1276 gggagagagctgancatgaaagcaagctgctgaaagctgctgcttcttctcctg 1335
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 601 GGTGAGAGCTGAAATAATGAACAAGCGCTTTGAGCTCTTCACTGTTACATCATCAGCT 660
Qy 1336 gaaccacacgggaatgctcaaaagctgctgctgctgctgaaagctgacccctggcg 1395
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 661 CAGCAAAACCAAGATGACCAAGATGATGTTACCAATGAGAGAGACCTCTGGCT 720
Qy 1396 gctgaagcagcagctgctgaaggaagagctgctgctgctgaaagcagcgagc 1449
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Db 721 CCAGAGACGAACCTCTGGAAGATCAGCTAGAAAAGTGAACACAGAGCGCTC 774

RESULT 9
AM050775/c 537 bp mRNA linear EST 20-SEP-1999
LOCUS W2210.10.1 Soares, Dieckgraefe, colon, NHCD Homo sapiens cDNA clone
DEFINITION IMAGE:2558706.3, similar to SM:MTFR_HUMAN P42898
METHLENTETRAHYDROFOLATE REDUCTASE ;, mRNA sequence.
ACCESSION AM050775 GI:5913045
VERSION AM050775
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
          Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 537)
AUTHORS NCI-CCGAP http://www.ncbi.nlm.nih.gov/ncicgap.
          National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
          Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
          Email: cgapbs-r@mail.nih.gov
          This clone is available royalty-free through LNL; contact the
          IMAGE Consortium (info@image.lnl.gov) for further information.
          Seq primer: -40UP from Glibco
          High quality sequence stop: 357.
          Location/Qualifiers
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            /db_xref="taxon:9606"
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            /tissue_type="colonic mucosa from 3 patients with Crohn's
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            /lab_host="DH10B (phage-resistant)"
            /note="Organ: colon; Vector: pTZ19-Pac (Pharmacia) with a
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            strand cDNA was primed with a Not I - oligo(dT) primer [5'
            TGTTCACATCTGAAAGTGGAGCGCGCGCTTTTCTTTTCTTTTCTTTTCTTTT
            3'],
            double-stranded cDNA was ligated to Eco RI adaptors
            (Pharmacia), digested with Not I and cloned into the Not I
            and Eco RI sites of the modified pTZ19 vector. Library
            went through one round of normalization. Tissue samples
            provided by Dr. Brian Dieckgraefe (Washington University,
            dieckelm.wustl.edu); colonic mucosa represents a range of
            disease; involvement from moderate to severe Crohn's
            disease; samples include both perforating (fistulas) and
            non-perforating samples. Library constructed by Bento
            Soares and M. Fatima Bonaldo.
BASE COUNT 116 a 134 c 171 g 116 t
ORIGIN

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Query Match 19.8%; Score 433.8; DB 9; Length 537;
Best Local Similarity 93.6%; Pred. No. 9.4e-85;
Matches 497; Conservative 0; Mismatches 27; Indels 7; Gaps 4;
Qy 1672 ctgcagccgaatgctgctcactgaggca--tcttccctggcgagagatca---ttcagc 1726

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Db 537 CTGCAAGCAATGCTTTTATTGGGGAATTTCCCTCGGGGAAAAATCATATCCAGC 478
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Db 477 CCACGAAATGATCCGGGTCAGCTTTCAGAGTTTGGAAAGAGACGAGGGCTTCCCTGTGG 418
Qy 1786 attgaagcgtgggaagcctgatatgaggaagagtcctccgctccgacattatccagtac 1845
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Db 417 ATTGAGCGGTGGGAAAGCTGTATGAGAGAGTCCCGCTCCGACCATCATCATCAGTAC 358
Qy 1846 atccagcaactactctcctgctacacctggttgacaatgactccacatggaacatgctc 1905
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Qy 1906 ctctgcaagctgctgaaagacacatctggaagctctcacaagccacccaagatgcgaga 1965
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Db 298 CTCTGCGAGGTGGTGGAAACACATTGGAGCTTCTCAACAGGCCACCAAGAAATGGCAGA 239
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RESULT 10
LOCUS BF654483 457 bp mRNA linear EST 25-APR-2001
DEFINITION 278682 MARC 3BOV Bos taurus cDNA 5', mRNA sequence.
ACCESSION BF654483
VERSION BF654483.1 GI:11919615
KEYWORDS EST.
SOURCE cow.
ORGANISM Bos taurus
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
          Bovidae; Bovinae; Bos.
REFERENCE 1 (bases 1 to 457)
AUTHORS Smith,T.P.L., Grosse,W.M., Freking,B.A., Roberts,A.J., Stone,R.T.,
          Casas,E., Wray,J.E., White,J., Cho,J., Fahrenkrug,S.C., Bennett
          G.L., Heaton,M.P., Laegreid,W.M., Rohrer,G.A., Chitko-McKown,C.G.,
          Keeler,G., Holt,I., Karamycheva,S., Liang,F., Quackenbush,J. and
          Keeler,J.W.
          Sequence evaluation of four pooled-tissue normalized bovine cDNA
          libraries and construction of a gene index for cattle
          Genome Res. 11 (4), 626-630 (2001)
JOURNAL 21180013
MEDLINE Contact: Smith TPL
COMMENT USDA, ARS, US Meat Animal Research Center
          PO Box 166, Clay Center, NE 68913-0166, USA
          Tel: 402 762 4366
          Fax: 402 762 4390
          Email: smitht@mail.marc.usda.gov
          Single pass sequencing. Bases called and alt-trimmed with phred
          v0.980904.e. Vector identified by cross-match with the -minscore 18
          and -mismatch 12 options.
PCR Primers
FORWARD: AGGAACAGCTATGACAT
BACKWARD: GTTTCACATGACGACG
Plate: 71 row: K column: 15
Seq primer: ATTAGTGACACTATAG.
          Location/Qualifiers
FEATURES

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TITLE
JOURNAL
MEDLINE
COMMENT

Nagai, M.A., da Silva, M. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Bata, G.S., Simpson, D.H., Brunstein, A., de Oliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and Simpson, A.J.

Shotgun sequencing of the human transcriptome with ORF expressed sequence tags

Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)

20202663

Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil

Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br

This sequence was derived from the PAPER/P/LICR Human Cancer Genome Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=MR2&cl=MR2-NT0135-211200-017-H09&cl3=2000-12-21&cl4=1)

Seq primer: puc 18 forward
High quality sequence stop: 400.

FEATURES
Source
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/db_xref="taxon:9606"
/clone_lib="NT0135"
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/note="Organ: nervous_tumor; Vector: puc18; Site_1: Sma1; Site_2: Sma1; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the puc 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

BASE COUNT
ORIGIN
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Query Match
Best Local Similarity 16.0%; Score 352.4; DB 10; Length 400;
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QY 71 gcaatgacatgagagctcccaagaatgctgagatgtccaccccgagctgagaccctg 130
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QY 131 agggagcagtagagatccggagagagatgagggcgagcttggaatctggtgacaagtgt 190
DB 85 AGCGGCGATGAGAGACTCCGGGAGAGATGAGCGCGGCGATTGGAATCTGTGACAAAGTGT 144

QY 191 tctccctggaattctccctccctcgaaactgctgagggagctgtcaatctcatcgaagt 250
DB 145 TCTCCCTGGAATCTCTCCCTCCCTCGAAGCTGCTGAGGAGCTGTCAATCTCATCTCAAGGT 204

QY 251 ttgacggatgagcagcaggtgtgcccctctacatagacgtgacctgtgacccagcaggtg 310
DB 205 TTGACGGATGAGCAGCAGGTGTGCCCCCTCTACATAGACGTGACCTGCGACACCAAGAGTGT 264

QY 311 accctgctcagaagaagaacctctctcctcagatgagcagcagcagcagcagcagcagcagc 370
DB 265 ACCCTGCTCAGCAAGAGAAAGAACTCTCTCCATGATGATGCGCAGACCGCGCTGAATCTACT 324

QY 371 gtggcctggaacacatcctcagatgacgtgtgctgacgagcagcagcagcagcagcagcagc 424
DB 325 GTGGCCTGGAGACCATCTCAGATGACCTGTGCGCTCAGCGCTGAGAGAGA 378

RESULT 13
LOCUS
DEFINITION

BM089718 549 bp mRNA linear EST 19-NOV-2001
BM089718
503548 MARC 2BOV Bos taurus cDNA 5', mRNA sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
MEDLINE
COMMENT

BM089718
BM089718.1 GI:17000346
EST.
Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovidae; Bovinae; Bos.

1 (bases 1 to 549)
Smith, T.P.L., Grosse, M.M., Freking, B.A., Roberts, A.J., Stone, R.T., Casas, E., Wray, J.E., White, J., Cho, J., Fahrenkrug, S.C., Bennett, G.L., Heaton, M.P., Laegreid, W.W., Rohrer, G.A., Chitko-Mckown, C.G., Pettea, G., Holt, I., Karamycheva, S., Liang, F., Quackenbush, J. and Keele, J.W.

Sequence evaluation of four pooled-tissue normalized bovine cDNA libraries and construction of a gene index for cattle

Genome Res. 11 (4), 626-630 (2001)

2118013

Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
Email: smith@email.marc.usda.gov

Single pass sequencing. Bases called and alt. trimmed with phred v0.980904.e. Vector identified by cross_match with the -minscore 18 and -mismatch 12 options.

PCR primers
FORWARD: AGGAACAGCTATGACCAT
BACKWARD: GTTTCCTCAGTCAGCAGC
Plate: 5 row: D column: 9
Seq primer: ATTGAGGTGACATCATGAG.

FEATURES
Source
1. 549
/organism="Bos taurus"
/db_xref="taxon:9913"
/clone_lib="MARC 2BOV"
/tissue_type="pooled"
/lab_host="DH10B"
/note="Vector: PCMV SPORT6; Site_1: Xba1; Site_2: Xho1; Library made from pooled tissue from testis, thymus, semitendinosus muscle, longissimus muscle, pancreas, adrenal, and endometrium."

BASE COUNT
ORIGIN
112 a 166 c 149 g 122 t

Query Match
Best Local Similarity 15.1%; Score 332; DB 10; Length 549;
Matches 353; Conservative 0; Mismatches 36; Indels 0; Gaps 0;

QY 593 tggcaggttaccaccaaggccaccggaagcagcagcttgtagctgagctgagcagcact 652
DB 161 TGGCAGGTTCACCCCAAAAGCCACCTTGAAAGAGAGAGCTTTGAGGCTGATGTAAGCAC 220

QY 653 tgaaggaaggtgttntcgagagcagattcatcatcaacgacagcttctcttgaggtgt 712
DB 221 TGAAGGAGAAAGTGTGCTGAGAGCCGACCTTCATCATCACCACCTATTTCTTGAGGCTG 280

QY 713 acaatctcttcgcttctgtgaagagcagcagcagcagcagcagcagcagcagcagcagcagc 772
DB 281 AACAATCTCTCCGCTTGTGAAGGCTTGCTCGAGATGAGCATTAACCTGCCCCATCTCC 340

QY 773 ccgggactcttcccatcagagctacacactcccttcggcagcagctgtgaagctgccaagc 832
DB 341 CCGGACTCTTCCCAATTCAGAGGCTACCACTCTCTCCGCACTGTGTAATCTCTCAAC 400

QY 833 tgaagtgccacagagagatcaagagcgttgatgagcacaatcaacgaacagatgctgcca 892
DB 401 TGAAGTGTCCACAGACAGATCAAGAGATGATGATGAGCCCATCAAGACAAATGATCTGCA 460

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Db 461 TCCGCAACTATGCGATCGAGCGCCGTGTGCCAGAGAGCTGTGCGCAATGAGCT 520
OY 953 Tggtcagagccctccactctacacccctc 981
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Db 521 TGGTCCAGAGCGCTCCACTCTACACCCCTC 549

RESULT 14
AA183742          499 bp  mRNA  linear  EST 15-FEB-1997
LOCUS             mo55c06.r1 Stratiagene mouse testis (#937308) Mus musculus cDNA
DEFINITION        clone IMAGE:567466 5' similar to WP:006A8.1 CE02451'', mRNA
SEQUENCE
ACCESSION         AA183742
VERSION           AA183742.1 GI:1767323
KEYWORDS          house mouse.
SOURCE            Mus musculus
ORGANISM          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                  Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE         Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
                  Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
                  Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
                  Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
                  Waterston,R.
TITLE             The Washu-HHMI Mouse EST Project
JOURNAL           Unpublished (1996)
COMMENT           Contact: Marra M/Mouse EST Project
                  Washu-HHMI Mouse EST Project
                  Washington University School of Medicine
                  4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
                  Tel: 314 286 1800
                  Fax: 314 286 1810
                  Email: mouseest@watson.wustl.edu
                  This clone is available royalty-free through INLTL; contact the
                  IMAGE Consortium (info@image.llnl.gov) for further information.
                  MGI:342114
                  Seq primer: -28m13 rev1 ET from Amersham
                  High quality sequence stop: 439.
FEATURES
    source
        1..499
            /organism="Mus musculus"
            /strain="Inbred CD-1"
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            /clone="IMAGE:567466"
            /clone_1lb="Stratiagene mouse testis (#937308)"
            /sex="males"
            /tissue_type="testis"
            /dev_stage="10-12 week old"
            /lab_host="SOLR (kanamycin resistant)"
            /note="Organ: testis; Vector: pBluescript SK-; Site_1:
            EcorI; Site_2: XhoI; Cloned unidirectionally. Primer:
            0190 dt. Average insert size: 1.0 kb; Uni-ZAP XR Vector:
            -5' adaptor sequence: 5' GAATTCGCGACGCG 3' -3' adaptor
            sequence: 5' CTCGAGTTTCTTTTCTTTTCTTTT 3'"
BASE COUNT        117 a 138 c 143 g 100 t 1 others
ORIGIN
Query Match      14.7%; Score 321.8; DB 9; Length 499;
Best Local Similarity 83.3%; Pred. No. 3.2e-60;
Matches 378; Conservative 0; Mismatches 73; Indels 3; Gaps 1;
OY 1532 tcttcagaagcctactagatttctactcccgagagcagcgagacactctgc 1591
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1 TCTTCCAAAGGCGCTACCTCGAATTCCTCACCCTCCGTCGAACGTGAGGCGCTTGC 60
OY 1592 aagtgctagaagagcagcgctccgggttaattaccacctgtcaatgtgaagggtga 1651
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 61 AGGTCCTAAGACATACGAGCGTGGGTCACACTACCATCTCGGAGCGTGAAGAGAGA 120
OY 1652 acatcaccaatgcctcgaatcagcgagcgaatgcgtcacttggtggcattcttcctgagc 1711

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Db 121 ACATCACTAATGCGCCCTGAGCTGCACGCCAATGCCCTGACGTGGGCGCATCTTCCGGGTC 180
OY 1712 gaggatcatcagccaccacgtagtgcacccgctcagcttcattctggaaggagag 1771
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 181 GAGAGATCATCCAGCCTACTGTGTGTGAGCCCACTACGCTTCATGTTCTGGAAGATGAGG 240
OY 1772 ccttgccctgtagattgagcggtgaggaaagctgtatgaggaaggagcccgctccga 1831
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 241 CCTTCCCTGTGGATGAGCAGTAGTGGGCAAGCTATACGAGGAGAGTGCCTCCCGCA 300
OY 1832 ccatcatcagtaacatccacagcaactactctctgtgtcaacctgtgtgagcaatgattcc 1891
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 301 TGATCATCCAAATACATCCATGACCAACTATTCTGTGCAACCTGTGGAACAGAGCTCC 360
OY 1892 cactgacacactgcctctgcaggtgtgtgaaagacacatgtgagctcacaagcgcca 1951
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Db 361 CGCTGACACGCTGCGCTGTGACAGNTGTGTGAGACACGTTTGAGCTGCTCAACAGGCATC 420
OY 1952 cccgaatgcgaggaagacgaggtccatgacc 1985
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Db 421 CC---ACGAGAGAGAGACACAGGCTCATGAGC 451

RESULT 15
BE753120          550 bp  mRNA  linear  EST 25-APR-2001
LOCUS             206029 MARC 2BOV Bos taurus cDNA 5', mRNA sequence.
DEFINITION        BE753120
ACCESSION         BE753120
VERSION           BE753120.1 GI:10167112
KEYWORDS          EST.
SOURCE            cow.
ORGANISM          Bos taurus
                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                  Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
                  Bovidae; Bovinae; Bos.
REFERENCE         Smith,T.P.L., Grosse,W.M., Freking,B.A., Roberts,A.J., Stone,R.T.,
                  Casas,E., Wray,J.E., White,J., Cho,J., Falkenkrug,S.C., Bennett
                  G.L., Heaton,M.P., Laegreid,W.M., Rohrer,G.A., Chitko-McKown,C.G.,
                  Perteau,G., Holt,I., Karamycheva,S., Liang,F., Quackenbush,J. and
                  Keele,J.W.
TITLE             Sequence evaluation of four pooled-tissue normalized bovine cDNA
                  libraries and construction of a gene index for cattle
JOURNAL           Genome Res. 11 (4), 626-630 (2001)
MEDLINE           21180013
COMMENT           Contact: Smith TPJ
                  USDA, ARS, US Meat Animal Research Center
                  PO Box 166, Clay Center, NE 68933-0166, USA
                  Tel: 402 762 4366
                  Fax: 402 762 4390
                  Email: smitht@mail.marc.usda.gov
                  Single pass sequencing. Bases called and alt_trimmed with phred
                  v0.980904.e. Vector identified by cross_match with the -m1nscore 18
                  and -m1match 12 options.
                  PCR Primers
                  FORWARD: AGGAACACGATGACCAT
                  BACKWARD: GTTTCCTCCAGTCACGAGC
                  Plate: 47 row: K column: 9
                  Seq primer: ATTAGTGACCATATAG.
FEATURES
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            /lab_host="DH10B"
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            library made from pooled tissue from testis, thymus,
            semitendinosus muscle, longissimus muscle, pancreas,
            adrenal, and endometrium."
BASE COUNT        116 a 172 c 173 g 89 t
ORIGIN

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